Fig. 1

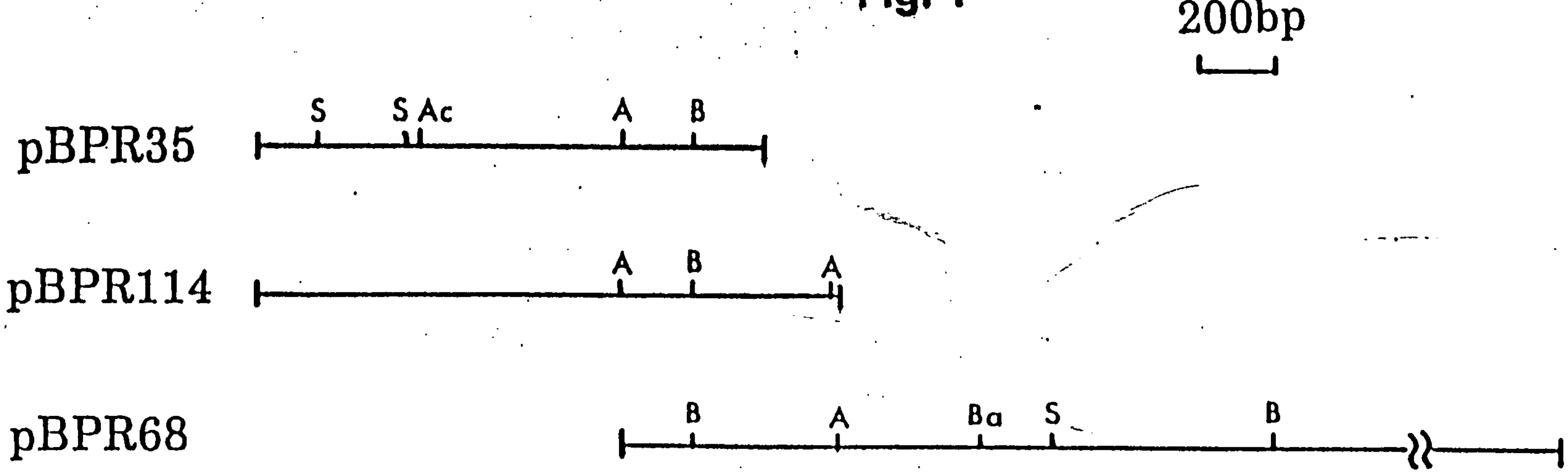

Fig. 2

1 TGGCCTGCACCCCACCCCCCAG[illegible]TGCGAAGACGGGGGGAGGCGGTGGTCGGTCGCCTCCCTCCTGCCC[illegible]CGGCCTGGCTTCGCGGTGGAG 91

92 GCGGTGCCTCTCCGGCAAGGCAGACCAGGCTGGGCGGACGCGCGGCGCGGGGCGGGCTAGGGAAGGCCGGGGGCCTCGCGCTCGGGCCCCGG 183

184 GCGGCGACTGACAGCGGCGGCGGCGGCGGCAGCGGCTCCAAGGCGAGCGTGGTCCCCGCGTGCGCACAAGCTCGCCGCCGCGCAGGGACCCA 275

276 CGGACACCGGCGCCGGGCGGACACACAGACGCGGAGATCGGGCTCTACGCGCGCTACTCAGCGCACGAGCTCCCCATCCCTGGGCGGAGCGG 367

368 GGCGCGGACTCGCCGCTGCGCGCCCTCCCCGCGGAGTCTGCCCCGGGCAGACCCCGCAGCCCCGCGGCCCCCGCCGAGGCCCCTGGGTGAGCA 459

1 Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg 13
460 GCCTGTAGACACCTGGGGTTGAGCAGTGGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG 536

14 Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr 36
537 CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC 605

37 Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn 59
606 GCC ATG CAT TCC GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT 674

60 Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys 82
675 GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG 743

83 Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln 105
744 CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA 812

106 Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met 128
813 GTC TGG GAG ACC GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG 881

129 Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys 151
882 AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT 950

152 Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr 174
951 GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC 1019

175 Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys 197
1020 ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG 1088

198 Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val 220
1089 CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC 1157

221 Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys 243
1158 TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC 1226

244 Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu 266
1227 AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG 1295

267 Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile 289
1296 TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT 1364

290 Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly 312
1365 GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC 1433

313 Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met 335
1434 TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG 1502

336 Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly 358
1503 GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA 1571

359 Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln 381
1572 GGC AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT CAG CAG 1640

382 His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile 404
1641 CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC 1709

405 Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu 427
1710 CCA CTC TTT GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG 1778

428 Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly 450
1779 GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA 1847

451 Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe 473
1848 GAG GTG CAG GCG GAG ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC 1916

474 Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys 496
1917 AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG 1985

497 Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr *** 513
1986 AGC AGC TCC CAG ATC CGC ATG TCT GGC CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCCACCCTGCCCCCTCCTC 2059

2060 TCCTCTGTACGCAGGCTGGGGCTGTGGTGGGGCGCCGGCCCACGCATGTTGTGCCTCTTCTCGCCTTCGGGCAGGCCCCGGCCTGGCGCCCT 2151

2152 GGCCCCCGAGGTTGGAGAAGGATGCGGGACAGGCAGCTGTTTAGCCTTCCTGTTTTGGCGCTGGCCCAACCACCGTGGGTCCCTGGGCCTGC 2243

2244 ACCCAGACATGTAATACTCCTTAATTGGGAAGTCATCCATTCTTTCCCTTTCCCAAGTCCTTGCTTATTAAGAGGTTCAAGTCACCTACCCA 2335

2336 ATTCAGAAGCTTAAGTAACCACTAACCACCGTGACTGCGTGGCAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCT 2427

2428 GGGGCCCTCCTTAAAGCCCCCCCTGAAATTGTCGGACCTCAAAGTGTGACTCCTTTGAGTCTACTCGCCACCCCCGTGGCCCTTTGCAGCCC 2519

2520 TGGTCCAGTCACCGAGGTTACTGGAAGTCCAGCTTGGATGGCCAGACAGCTTTTTGGCACAGGCAGACCCATGCTCACCCAACATTTTAGTG 2611

2612 TCCAGGTGCCCAGGTGCCCAGGTGCCCAGCTCCTGGGCATCAGACAGTGGCAAAGCTCCAGGGATCTACCATTCAGAGACTTCAGTTTGGAT 2703

2704 GTAGGGCTAAGGCCAGAGAAAAGTTCTGGAGCTTTTCATTTGGCCCAAGAAAAAACTGCCAAGATCCAGAAAAGTGGATCTGAGTGGAATTT 2795

2796 AGATGCAAAGAGCTTGGAG 2814

Fig. 3

```
1    TGGCCTGCACCCCACCCCCCAGCCTGCGAAGACGGGGGGAGGCGGTGGTCGGTCGCCTCCCTCCTGCCCCCCGCCCTGGCTTCGCCGTCGAG    91
92   GCGGTGCCTCTCCGGCAAGGCAGACCAGGCTGGGCGGACGCCGCGCCCCGGGGCGGGCTAGGGAAGCCCCGGGGGCCTCGCCGCTCGGGCCCCCG    183
184  GCGGCGACTGACAGCGGCGGCGGCGGCGGCAGCGGCTCCAAGGCGAGCGTGGTCCCCGCGTGCGCACAAGCTCGCCGCCGCGCAGGGACCCA    275
276  CGGACACCGGCGCCGGGCGGACACACAGACGCGGAGATCGGGCTCTACGCGCGCTACTCAGCGCACGAGCTCCCCATCCCTGGGCCGAGCGG    367
368  GGCGCGGACTCGCCGCTGCGCGCCCTCCCCGCGGAGTCTGCCCCGGGCAGACCCGCAGCCCCGCGGCCCCCCCCGCGAGCCCCCTGGGTGAGCA    459
1                                                Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg    13
460  GCCTGTAGACACCTGGGGTTGAGCAGTCGCGGCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT TGC AGG    536
14   Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr    36
537  CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC    605
37   Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn    59
606  GCC ATG CAT TCC GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT    674
60   Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys    82
675  GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG    743
83   Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln    105
744  CCC GCC CAC GTG GGT GAG ATG GTC CTG GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA    812
106  Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met    128
813  GTC TGG GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG    881
129  Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys    151
882  AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT    950
152  Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr    174
951  GGG TTT GAG GAG TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG GCC CTG TAC    1019
175  Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys    197
1020 ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG    1088
198  Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val    220
1089 CTG CAC TGC ACC CGC AAC TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC    1157
221  Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys    243
1158 TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC    1226
244  Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu    266
1227 AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG    1295
267  Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile    289
1296 TAT CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATC ATT    1364
290  Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly    312
1365 GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC    1433
313  Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met    335
1434 TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG    1502
336  Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly    358
1503 GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA    1571
359  Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile    381
1572 GGC AAC GAG TCC AGC ATC TAC TTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC    1640
382  His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly    404
1641 CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG GTG TTT GAG CTG GGT    1709
405  Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu    427
1710 CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG    1778
428  Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro    450
1779 ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC CGG CAC CCA    1847
451  Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile    473
1848 TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC    1916
474  Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***    485
1917 CGC ATG TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCCACCCTGCCCCCTCCTCTCCTCTGTACGCAGGCTGGG    1995
1996 GCTGTGGTGGGGCCCCGGCCCCACGCATGTTGTGCCTCTTCTCGCCTTCGGGCAGGCCCCGGGCTGGCCGCCTGGCCCCCGAGGTTGGAGAAG    2087
2088 GATGCGGGACAGGCAGCTGTTTAGCCTTCCTGTTTTGGCCGCTGGCCCAACCACCGTGGGTCCCTGGGCCTGCACCCAGACATGTAATACTCC    2179
2180 TTAATTGGGAAGTCATCCATTCTTTCCCTTTCCCAAGTCCTTGCTTATTAAGAGGTTCAAGTCACCTACCCAATTCAGAAGCTTAAGTAACC    2271
2272 ACTAACCACCGTGACTGCGTGGGAGGCCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCCTTGGGCTGGGGCCCTCCTTAAAGCCCC    2363
2364 CCCTGAAATTGTCGGACCTCAAAGTGTGACTCCTTTGAGTCTACTCGCCACCCCCGTGGCCCTTTGCAGCCCTGGTCCAGTCACCGAGGTTA    2455
2456 CTGGAAGTCCAGCTTGGATGGCCAGACAGCTTTTTGGCACAGGCAGACCCATGCTCACCCAACATTTTAGTGTCCAGGTGCCCCAGGTGCCCCA    2547
2548 GGTGCCCCAGCTCCTGGGCATCAGACAGTGGAAAGCTCCAGGGATCTACCATTCAGAGACTTCAGTTTGGATGTAGGGCTAAGGCCAGAGAA    2639
2640 AAGTTCTCGAGCTTTTCATTTGGCCCAAGAAAAAACTGCCAAGATCCAGAAAAGTGCATCTGAGTGGAATTTAGATGCAAAGAGCTTGGAG    2730
```

Fig. 4

	1				5					10	
Bovine cDNA	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln
	*	*	*	*	*	*	*	*	*	*	*
Purified bovine Sample	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln

			15					20					25
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met
*	*	*	*	*	*	*	*	*	*	*	*	*	*
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met

Gly	Leu	Asn	Asp
*	*	*	*
Gly	Leu	Asn	Asp

Fig. 5

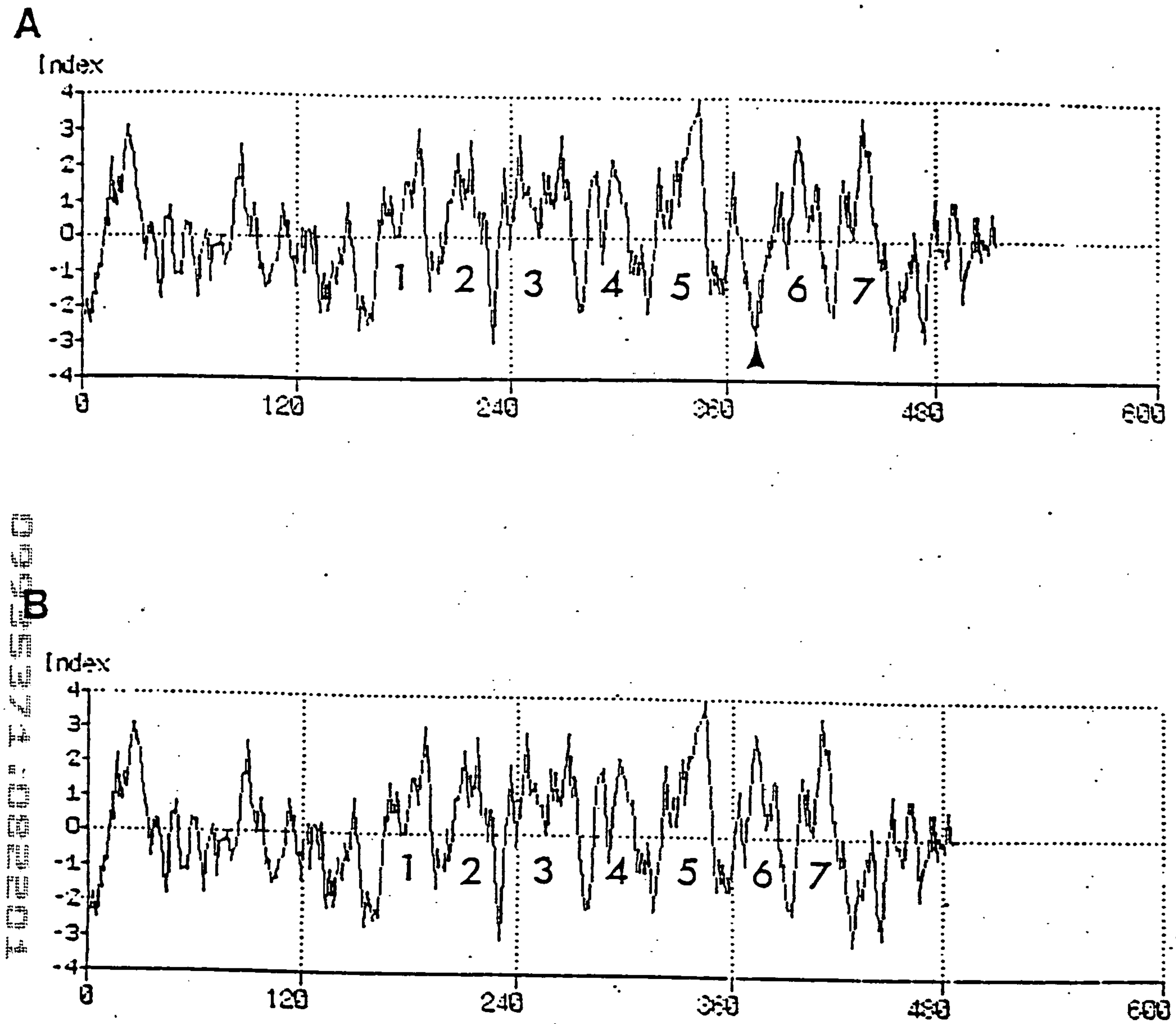
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Fig. 6

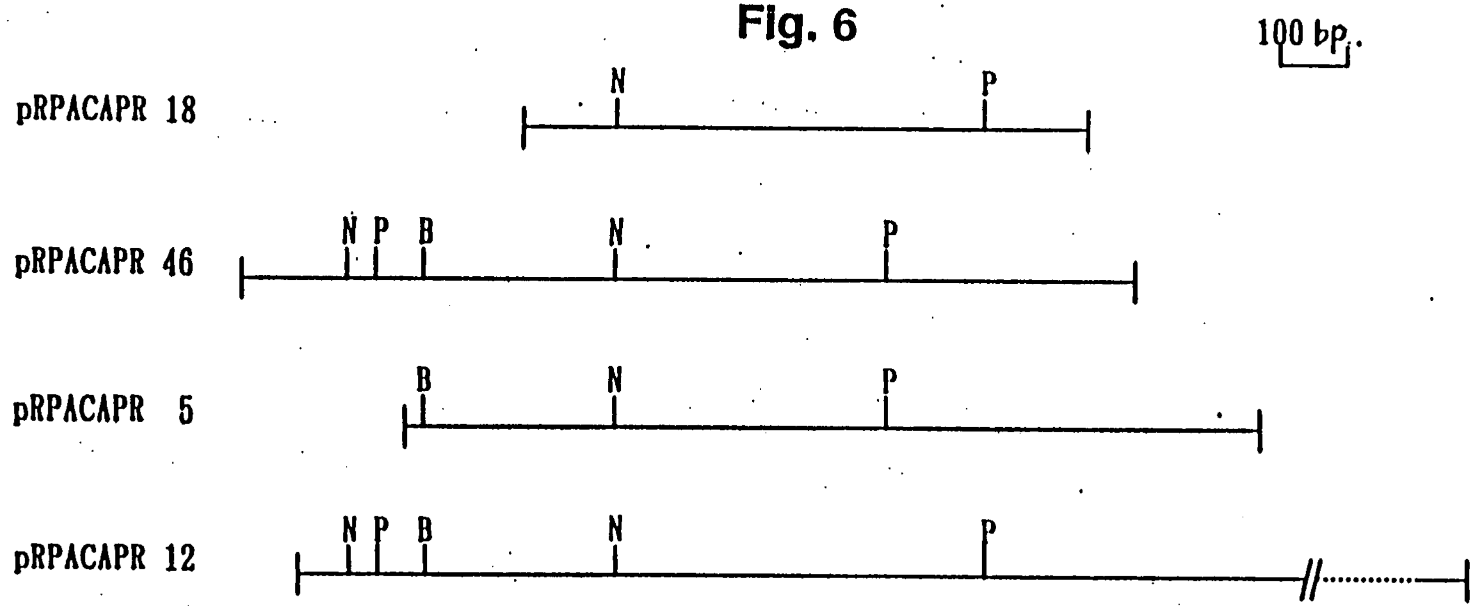

Fig. 7

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1    CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA   58

59   TAGTGGCTGGGAAGCACCATGGCCAGAGTCCTGCAGCTCTCCCTGACTGCTCTCCTGCTG 118
1                        MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu 14

119  CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG 178
15   ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu 34

179  GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT 238
35   GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro 54

239  GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA 298
55   GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal 74

299  AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA 358
75   SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle 94

359  GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC 418
95   GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly 114

419  CGGAACTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG 478
115  ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly 134

479  TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT 538
135  PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla 154

539  CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG 598
155  LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu 174

599  TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC 658
175  CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer 194

659  TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC 718
195  PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp 214

719  AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC 778
215  SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr 234

779  TGCGTGGTGTCCAACTACTTCTGGCTGTTCATTGAAGGCCTGTACCTCTTTACACTGCTG 838
235  CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu 254

839  GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG 898
255  ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly 274

899  ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA 958
275  ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly 294

959  TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC 1018
295  CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly 314

1019 TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCATCCTTGTACAGAAGCTG 1078
315  SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu 334

1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTACGGCTGGCCCGCTCCACC 1138
335  GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrLeuArgLeuAlaArgSerThr 354
```

Fig. 8

1139 CTACTGCTCATCCCACTCTTCGGAATCCACTACACAGTATTCGCCTTCTCTCCAGAGAAC 1198
355 LeuLeuLeuIleProLeuPheGlyIleHisTyrThrValPheAlaPheSerProGluAsn 374

1199 GTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGGCTGGGCTCCTTCCAGGGCTTTGTG 1258
375 ValSerLysArgGluArgLeuValPheGluLeuGlyLeuGlySerPheGlnGlyPheVal 394

1259 GTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTACAGGCAGAGATTAAGAGGAAATGG 1318
395 ValAlaValLeuTyrCysPheLeuAsnGlyGluValGlnAlaGluIleLysArgLysTrp 414

1319 AGGAGCTGGAAGGTGAACCGTTACTTCACTATGGACTTCAAGCACCGGCACCCGTCCCTG 1378
415 ArgSerTrpLysValAsnArgTyrPheThrMetAspPheLysHisArgHisProSerLeu 434

1379 GCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCCATCCTGAGCAAGAGCAGCTCCCAG 1438
435 AlaSerSerGlyValAsnGlyGlyThrGlnLeuSerIleLeuSerLysSerSerSerGln 454

1439 CTCCGCATGTCCAGCCTCCCGGCCGACAACTTGGCCACCTGAGGCCTGTCTCCCTCCTCC 1498
455 LeuArgMetSerSerLeuProAlaAspAsnLeuAlaThr*** 467

1499 TTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAGCATGTTTGTGCCTCTCCCCTCTCC 1558
1559 TTGGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCCCAAAGGGGAAGAGAGAGATAGGGT 1618
1619 ATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACCTACTGTGATTCATTGAGCCTGATT 1678
1679 TGACATGTAAATACACCTCAAATTTGGAAAGTTGCCCCATCTCTGCCCCCAACCCATGCC 1738
1739 CCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACTGTGTCAAGGCCAGCCTCAGTGATA 1798
1799 GTCTGATCCCAGGTACAAGGCCTTGTGAGCTGAGGCTGAAAGGCCTGTTTTGGAGAGGCT 1858
1859 GGGGTAGTGCC 1869

Fig. 9

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   1  CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA    58

  59 TAGTGGCTGGGAAGCACCATGGCCAGAGTCCTGCAGCTCTCCCTGACTGCTCTCCTGCTG  118
   1                   MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu   14

 119 CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG  178
  15 ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu   34

 179 GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT  238
  35 GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro   54

 239 GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA  298
  55 GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal   74

 299 AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA  358
  75 SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle   94

 359 GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC  418
  95 GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly  114

 419 CGGAACTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG  478
 115 ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly  134

 479 TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT  538
 135 PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla  154

 539 CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG  598
 155 LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu  174

 599 TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC  658
 175 CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer  194

 659 TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC  718
 195 PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp  214

 719 AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC  778
 215 SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr  234

 779 TGCGTGGTGTCCAACTACTTCTGGCTGTTCATTGAAGGCCTGTACCTCTTTACACTGCTG  838
 235 CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu  254

 839 GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG  898
 255 ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly  274

 899 ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA  958
 275 ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly  294

 959 TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC 1018
 295 CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly  314

1019 TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCATCCTTGTACAGAAGCTG 1078
 315 SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu  334

1079 CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTCAGCTGCGTGCAGAAATGC 1138
 335 GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrPheSerCysValGlnLysCys  354
```

Fig. 10

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1139 TACTGCAAGCCACAGCGGGCTCAGCAGCACTCTTGCAAGATGTCAGAACTATCCACCATT 1198
 355 TyrCysLysProGlnArgAlaGlnGlnHisSerCysLysMetSerGluLeuSerThrIle  374

1199 ACTCTACGGCTGGCCCGCTCCACCCTACTGCTCATCCCACTCTTCGGAATCCACTACACA 1258
 375 ThrLeuArgLeuAlaArgSerThrLeuLeuLeuIleProLeuPheGlyIleHisTyrThr  394
        △

1259 GTATTCGCCTTCTCTCCAGAGAACGTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGG 1318
 395 ValPheAlaPheSerProGluAsnValSerLysArgGluArgLeuValPheGluLeuGly  414

1319 CTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTA 1378
 415 LeuGlySerPheGlnGlyPheValValAlaValLeuTyrCysPheLeuAsnGlyGluVal  434

1379 CAGGCAGAGATTAAGAGGAAATGGAGGAGCTGGAAGGTGAACCGTTACTTCACTATGGAC 1438
 435 GlnAlaGluIleLysArgLysTrpArgSerTrpLysValAsnArgTyrPheThrMetAsp  454

1439 TTCAAGCACCGGCACCCGTCCCTGGCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCC 1498
 455 PheLysHisArgHisProSerLeuAlaSerSerGlyValAsnGlyGlyThrGlnLeuSer  474

1499 ATCCTGAGCAAGAGCAGCTCCCAGCTCCGCATGTCCAGCCTCCCGGCCGACAACTTGGCC 1558
 475 IleLeuSerLysSerSerSerGlnLeuArgMetSerSerLeuProAlaAspAsnLeuAla  494

1559 ACCTGAGGCCTGTCTCCCTCCTCCTTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAG 1618
 495 Thr***                                                        495

1619 CATGTTTGTGCCTCTCCCCTCTCCTTGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCC 1678
1679 CAAAGGGGAAGAGAGAGATAGGGTATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACC 1738
1739 TACTGTGATTCATTGAGCCTGATTTGACATGTAAATACACCTCAAATTTGGAAAGTTGCC 1798
1799 CCATCTCTGCCCCCAACCCATGCCCCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACT 1858
1859 GTGTCAAGGCCAGCCTCAGTGATAGTCTGATCCCAGGTACAAGGCCTTGTGAGCTGAGGC 1918
1919 TGAAAGGCCTGTTTTGGAGAGGCTGGGGTAGTGCCCACCCCAGCAGCCTTTCAGCAAATT 1978
1979 GACTTTGGATGTGGACCCTTCTCAGCCTGTACCAAGTACTGCAGTTGGCTAGGGATGCAG 2038
2039 CTCAGTTTCCTGAGCATCCTTTGGAGCAGGTCAACCTGAGGCTCCTTTTGCTTACCCGAC 2098
2099 ATCTAAGTTGTCCAGGTGCTCGGCTCCTGTGTGCCTGGATGACGGGAGGGCTCCGGGGTC 2158
2159 TTTCAGTCAAAGACTTACATTGAGGTGGGGTGAGAGTCAGAGAAAAGTTCTGGTGCTTTT 2218
2219 CATTTGTTCTAAGAGCTGAGAGCCAGGAATGCAGAGTCAATTGGGAAGGAGATGGGATAG 2278
2279 CTGATGATCTTACCATGTCCATGACTGTGCCCCTGATTCAAGACCGGATCATGTGGTGGC 2338
2339 TTTATTTCTACACTTCTTGTCCACAATGGACAGTCTGAGGAAGCTCTTCTTTCAGCCACA 2398
2399 ACAACCACAGAAAGCCCTTTCTTCTCCCCTCTTGTTTCTCCATAAGTCAAAGCCATGTTT 2458
2459 AGAACGGACCAGCCACCTTGCGATGAAATCACTGAGTTCTGAAGCAACTTTCAATTTCCA 2518
2519 CGAGCCAAGTCCTGGGTCCAGGACGCCCC                                 2548
```

Fig. 11

Rat	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	1				5					10					15	

Rat	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu
		*	*	*		*	*	*	*	*	*	*	
Bovine	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp
				20					25				

Fig. 12

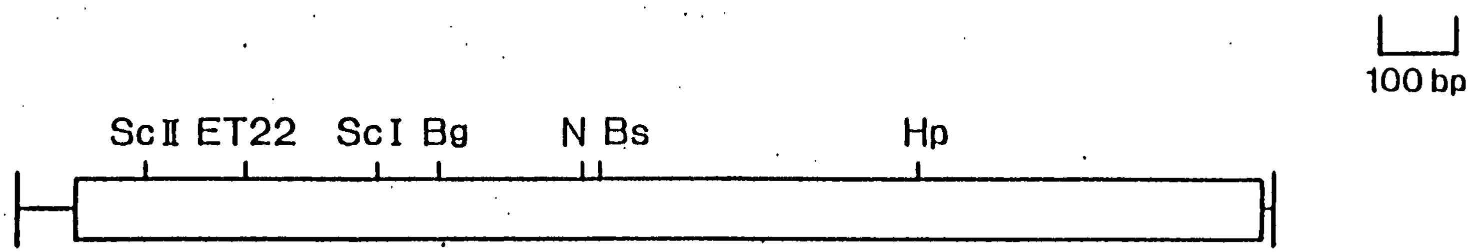

Fig. 13

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1    AGCCCAGAGACACATTGGGGCTGACCTGCCGCTGCTGTCAGTGGGAGGCCAGTGGTGCTGGCCAAGAAGTGTC ATG   76
1                                                                              Met    1

77   GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC   136
2    Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly   21

137  AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC   196
22   Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp   41

197  CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC   256
42   Leu Pro Leu Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val   61

257  GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC   316
62   Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp   81

317  TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG   376
82   Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu   101

377  ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG   436
102  Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp   121

437  AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC TTC   496
122  Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe   141

497  AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC AGT AAC   556
142  Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser Asn   161

557  TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG   616
162  Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser   181

617  GAA CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG   676
182  Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly   201

677  GAC CAG GAT TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC   736
202  Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser   221

737  CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA   796
222  Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr   241

797  CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC   856
242  Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe   261

857  ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG   916
262  Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val   281

917  GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG CTG   976
282  Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu   301

977  TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG AGA   1036
302  Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg   321

1037 TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG   1096
322  Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp   341

1097 GCT ACG CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT   1156
342  Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala   361

1157 CTG TGG TGG GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT   1216
362  Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe   381

1217 ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG   1276
382  Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu   401

1277 TCC AGC ATC TAC TTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC   1336
402  Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile   421

1337 CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT   1396
422  His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe   441

1397 GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT   1456
442  Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn   461

1457 GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC TTC   1516
462  Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe   481

1517 GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC ACC   1576
482  Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr   501

1577 CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC   1636
502  Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp   521

1637 AAT CTG GCC ACC TGA GCCATGCTCCCCT                                                 1664
```

Fig. 14

					5					10					15
Human	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu

					20					25				
Human	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp
	*	*	*	*	*		*		*	*	*		*	*
Bovine	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp

Fig. 15

Rat	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
TypeI−B	AAC	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG
pHPR15A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
humanTypeI−B	AAT	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG
pHPR55A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	—	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
TypeI−B2	AAT	GAG	TCC	AGC	ATC	TAC	TTC		TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG
pHPR66P	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg	Val	Pro	Lys
TypeI−C	AAT	GAG	TCC	AGC	ATC	TAC	TTA	ACA	AAT	TTA	AGC	CCG	CGA	GTC	CCC	AAG

Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTA	TCC	ACC
Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC
Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC
Lys	Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln	His	Ser	Leu
AAA	GCC	CGA	GAG	GAC	CCC	CTG	CCT	GTG	CCC	TCA	GAC	CAG	CAT	TCA	CTC

Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTA	CGG	CTG	GCC	CGC	TCC	ACC	CTA
Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG
Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG
Pro	Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
CCT	TTC	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG

Fig. 16

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1       A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA      67

1             Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly      21
68    AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC     136

22    Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu      44
137   AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205

45    Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala      67
206   CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT     274

68    Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met      90
275   GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG     343

91    Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly     113
344   TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG     412

114   Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu     136
413   ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG     481

137   Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp     159
482   CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC     550

160   Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu     182
551   AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA     619

183   Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr     205
620   CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT     688

206   Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala     228
689   TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC     757

229   Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val     251
758   ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG     826

252   Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn     274
827   TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC     895

275   His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn     297
896   CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC     964

298   Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg     320
965   TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG    1033

321   Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr     343
1034  AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG    1102

344   Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile     366
1103  CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC    1171

367   Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val     389
1172  AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG    1240

390   Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys     412
1241  CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC    1309

413   Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg     435
1310  TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA    1378

436   Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro     458
1379  CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA    1447

459   Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val     481
1448  GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG    1516

482   Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys     504
1517  GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG    1585

505   Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly     527
1586  GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG    1654

528   Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn     550
1655  GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT    1723

551   Leu Ala Thr ***                                                                                 553
1724  CTG GCC ACC TGA GCC ATG CTC CCC T                                                              1748
```

Fig. 17

1 A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA 67

1 Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly 21

68 AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC 136

22 Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu 44

137 AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG 205

45 Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala 67

206 CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT 274

68 Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met 90

275 GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG 343

91 Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly 113

344 TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG 412

114 Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu 136

413 ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG 481

137 Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp 159

482 CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC 550

160 Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu 182

551 AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA 619

183 Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr 205

620 CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT 688

206 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala 228

689 TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC 757

229 Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val 251

758 ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG 826

252 Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn 274

827 TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC 895

275 His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn 297

896 CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC 964

298 Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg 320

965 TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG 1033

321 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr 343

1034 AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG 1102

344 Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile 366

1103 CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC 1171

367 Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val 389

1172 AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG 1240

390 Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr 412

1241 CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC 1309

413 Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu 435

1310 TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTG CGA CTG 1378

436 Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu 458

1379 GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG 1447

459 Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala 481

1448 AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT 1516

482 Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val 504

1517 GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG 1585

505 Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly 527

1586 AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG GGC 1654

528 Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu 550

1655 ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG 1723

551 Ala Thr *** 552

1724 GCC ACC TGA GCC ATG CTC CCC T 1745

Fig. 18

1 A GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA 67

1 Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys Pro Trp Gly Arg Gly 21
68 AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC TGC GGG GCC TGT CCG TGG GGC CGG GGC 136

22 Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu 44
137 AGA CTC CGC AAA GGA CGC GCA GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG 205

45 Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val Ser Leu Ala 67
206 CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT 274

68 Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met 90
275 GCT CTC CTC CTG CTG CCT ATG GCC CCT GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG 343

91 Cys Leu Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro Gly 113
344 TGC CTG GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT CCA GGC TGT CCT GGG 412

114 Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu 136
413 ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG 481

137 Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp 159
482 CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT TTT GGT GAC 550

160 Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu 182
551 AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA 619

183 Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr 205
620 CCC TTC CCT CAT TAC TTT GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT TAT 688

206 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala 228
689 TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA TCC CTC GTC ACC CTC ACC ACT GCC 757

229 Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val 251
758 ATG GTC ATC CTT TGT CGC TTC CGG AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG 826

252 Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn 274
827 TCG TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT GCG GAG CAG GAC AGC AAC 895

275 His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn 297
896 CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC 964

298 Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg 320
965 TAC TTC TGG CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC TTC CCT GAA AGG 1033

321 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr 343
1034 AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG 1102

344 Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile 366
1103 CTG AGA CTC TAC TTT GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG GTG ATC 1171

367 Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val 389
1172 AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT TTT ATT GGC ATT ATC GTC ATC CTT GTG 1240

390 Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg 412
1241 CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA 1309

413 Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu Pro Phe Leu Arg 435
1310 GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC CCT TTC CTG CGA 1378

436 Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro 458
1379 CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA 1447

459 Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val 481
1448 GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG 1516

482 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys 504
1517 GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG 1585

505 Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly 527
1586 GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG AAT GGG 1654

528 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn 550
1655 GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT 1723

551 Leu Ala Thr *** 553
1724 CTG GCC ACC TGA GCC ATG CTC CCC T 1748

Fig. 19

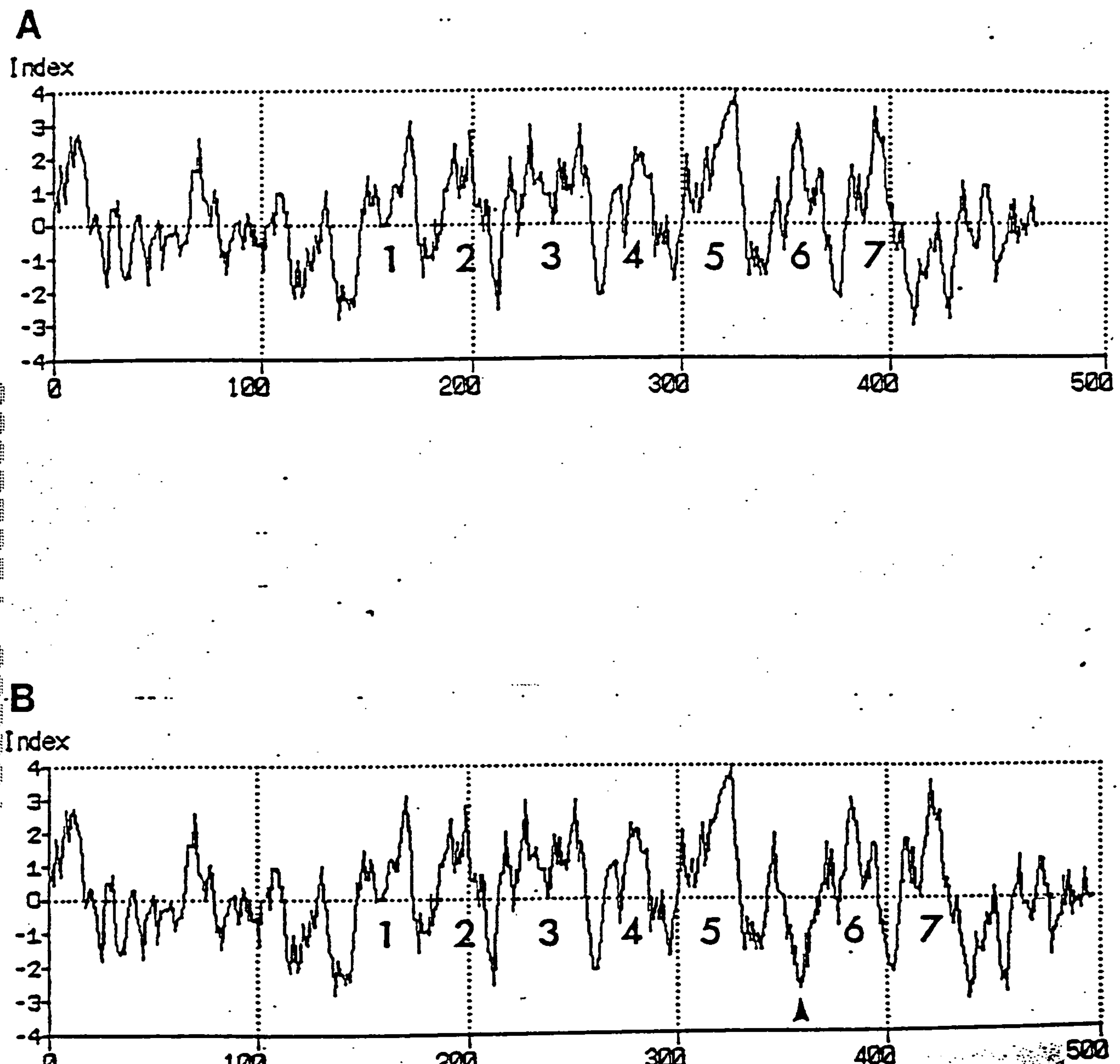
A
Index
4
3
2
1
0
-1
-2
-3
-4
0
100
200
300
400
500
1
2
3
4
5
6
7
B
Index
4
3
2
1
0
-1
-2
-3
-4
0
100
200
300
400
500
1
2
3
4
5
6
7

Fig. 20

```
EQUIVALENT
    1 : Ala(A),Ser(S),Thr(T),Pro(P),Gly(G)
    2 : Asn(N),Asp(D),Asx(B),Glu(E),Gln(Q),Glx(Z)
    3 : His(H),Arg(R),Lys(K)
    4 : Met(M),Leu(L),Ile(I),Val(V)
    5 : Phe(F),Tyr(Y),Trp(W)

PACAP receptor (upper lines)

VIP   receptor (lower lines)

      19        29        39        49        59        69        79
TALLLPVAIAMHSDCIFKKEQAMCLERIQRANDLMGLNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEV
  *  *         **   * *     *          * *     * *        **
MRPPSPPHVRWLCVLAGALACALRPAGSQAASPQHECEYLQLIEIQRQQCLEEAQLENETTGCSKMWDNL
      10        20        30        40        50        60        70

      89        99        109       119       129       139       149
FRIFNPDQVWMTETIGDSGFADSNSLEITDMGVVGRNCTEDGWSEPFPHYFDACGFDDYEPESGDQDYYY
    *          *   **  ***   * *    *  *  *           *  **  **
TCWPTTPRGQAVVLDCPLIFQLFAPIHGYNISRSCTEEGWSQLEPGPYHIACGLNDRASSLDEQQQTKFY
      80        90        100       110       120       130       140

      159       169       179       189       199       209       219
LSVKALYTVGYSTSLATLTTAMVILCRFRKLHCTRNFIHMNLFVSFMLRAISVFIKDWILYAEQDSSHCF
**** ****** *****  ** **  ************* ********* ******   **   *  **
NTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEIDHCS
      150       160       170       180       190       200       210

      229       239       249       259       269       279       289
VSTVECKAVMVFFHYCVVSNYFWLFIEGLYLFTLLVETFFPERRYFYWYTIIGWGTPTVCVTVWAVLRLY
*** *** **** ********** **********  ********** * ***** *** **********
EASVGCKAAVVFFQYCVMANFFWLLVEGLYLYTLLAVSFFSERKYFWGYILIGWGVPSVFITIWTVVRIY
      220       230       240       250       260       270       280

      299       309       319       329       339       349       359
FDDAGCWDMNDSTALWWVIKGPVVGSIMVNFVLFIGIIIILVQKLQSPDMGGNESSIYLRLARSTLLLIP
*** ****    ************ ********** ** ****** ***** **** * ***********
FEDFGCWDTIINSSLWWIIKAPILLSILVNFVLFICIIRILVQKLRPPDIGKNDSSPYSRLAKSTLLLIP
      290       300       310       320       330       340       350

      369       379       389       399       409       419       429
LFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLYCFLNGEVQAEIKRKWRSWKVNRYFTMDFKH
****** **** ***       ****** ***************************** ****   *   *
LFGIHYVMFAFFPDNFKAQVKMVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKS
      360       370       380       390       400       410       420

      439       449       459
RHPSLASSGVNGGTQLSILSKSSSQLRMSSLPADNLAT*
** ** *   ********* **  * **   ***
QHPWGGSNGATCSTQVSMLTRVSPSARRSSSFQAEVSLV
      430       440       450
```

Fig. 21

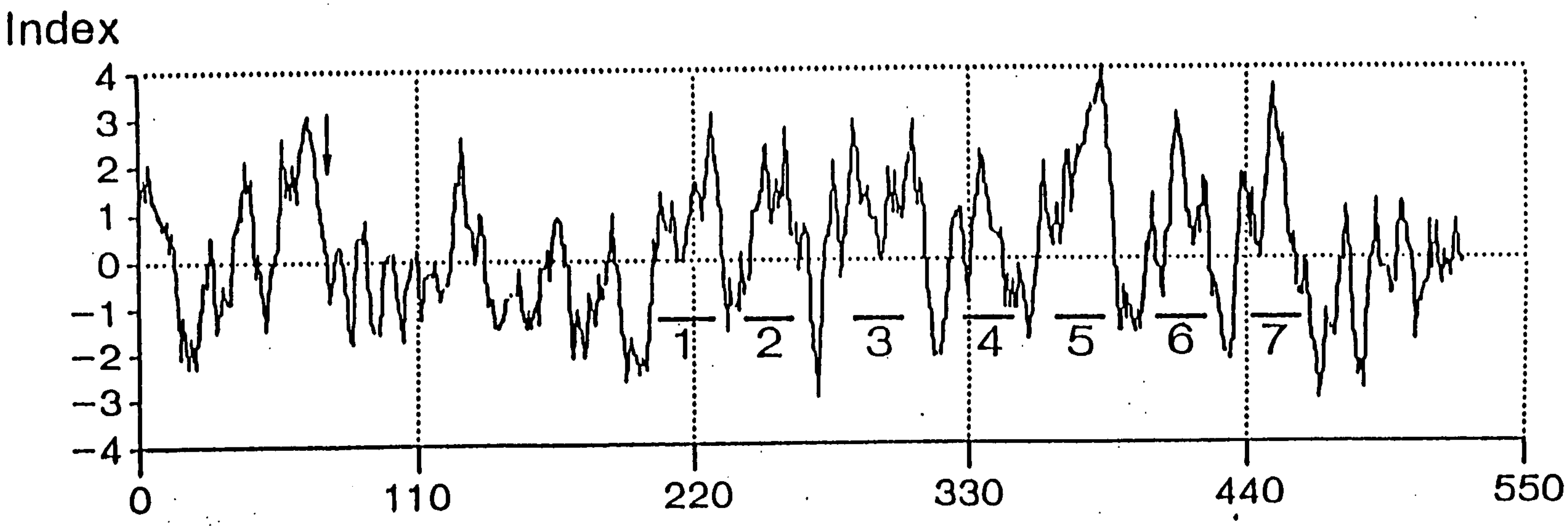

Fig. 22

```
                10          20          30          40          50          60          70          80
HUMAN    MAGVVHVSLA  AHCGACPWGR  GRLRKGRAAC  KSAAQRHIGA  DLPLLSVGGQ  WCWPRSVMAG  VVHVSLAALL  LLPMAPAMHS
BOVINE   ..........  ..........  ..........  ..........  MRGGRHWPEP  PCRLRSVMAS  IAQVSLAALL  LLPMATAMHS
RAT      ..........  ..........  ..........  ..........  ..........  .......MAR  VLQLSLTALL  L-PVAIAMHS

                90         100         110         120         130         140         150         160
         DCIFKKEQAM  CLEKIQRANE  LMGFNDSSPG  CPGMWDNITC  WKPAHVGEMV  LVSCPELFRI  FNPDQVWETE  TIGESDFGDS
         DCIFKKEQAM  CLEKIQRVND  LMGLNDSSPG  CPGMWDNITC  WKPAHVGEMV  LVSCPELFRI  FNPDQVWETE  TIGEFGFADS
         DCIFKKEQAM  CLERIQRAND  LMGLNESSPG  CPGMWDNITC  WKPAQVGEMV  LVSCPEVFRI  FNPDQVWMTE  TIGDSGFADS

               170         180         190         200         210         220         230         240
         NSLDLSDMGV  VSRNCTEDGW  SEPFPHYFDA  CGFDEYESET  GDQDYYYLSV  KALYTVGYST  SLVTLTTAMV  ILCRFRKLHC
         KSLDLSDMRV  VSRNCTEDGW  SEPFPHYFDA  CGFEEYESET  GDQDYYYLSV  KALYTVGYST  SLVTLTTAMV  ILCRFRKLHC
         NSLEITDMGV  VGRNCTEDGW  SEPFPHYFDA  CGFDDYEPES  GDQDYYYLSV  KALYTVGYST  SLATLTTAMV  ILCRFRKLHC

               250         260         270         280         290         300         310         320
         TRNFIHMNLF  VSFMLRAISV  FIKDWILYAE  QDSNHCFIST  VECKAVMVFF  HYCVVSNYFW  LFIEGLYLFT  LLVETFFPER
         TRNFIHMNLF  VSFMLRAISV  FIKDWILYAE  QDSNHCFVST  VECKAVMVFF  HYCVVSNYFW  LFIEGLYLFT  LLVETFFPER
         TRNFIHMNLF  VSFMLRAISV  FIKDWILYAE  QDSSHCFVST  VECKAVMVFF  HYCVVSNYFW  LFIEGLYLFT  LLVETFFPER

               330         340         350         360         370         380         390         400
         RYFYWYTIIG  WGTPTVCVTV  WATLRLYFDD  TGCWDMNDST  ALWWVIKGPV  VGSIMVNFVL  FIGIIVILVQ  KLQSPDMGGN
         RYFYWYIIIG  WGTPTVCVSV  WAMLRLYFDD  TGCWDMNDNT  ALWWVIKGPV  VGSIMVNFVL  FIGIIVILVQ  KLQSPDMGGN
         RYFYWYTIIG  WGTPTVCVTV  WAVLRLYFDD  AGCWDMNDST  ALWWVIKGPV  VGSIMVNFVL  FIGIITILVQ  KLQSPDMGGN

               410         420         430         440         450         460         470         480
         ESSIY-----  ----------  ----------  ---LRLARST  LLLIPLFGIH  YTVFAFSPEN  VSKRERLVFE  LGLGSFQGFV
         ESSIYFSCVQ  KCYCKPQRAQ  QHSCKMSELS  TITLRLARST  LLLIPLFGIH  YTVFAFSPEN  VSKRERLVFE  LGLGSFQGFV
         ESSIYFSCVQ  KCYCKPQRAQ  QHSCKMSELS  TITLRLARST  LLLIPLFGIH  YTVFAFSPEN  VSKRERLVFE  LGLGSFQGFV

               490         500         510         520         530         540         550
         VAVLYCFLNG  EVQAEIKRKW  RSWKVNRYFA  VDFKHRHPSL  ASSGVNGGTQ  LSILSKSSSQ  IRMSGLPADN  LAT
         VAVLYCFLNG  EVQAEIKRKW  RSWKVNRYFT  MDFKHRHPSL  ASSGVNGGTQ  LSILSKSSSQ  IRMSGLPADN  LAT
         VAVLYCFLNG  EVQAEIKRKW  RSWKVNRYFT  MDFKHRHPSL  ASSGVNGGTQ  LSILSKSSSQ  LRMSSLPADN  LAT
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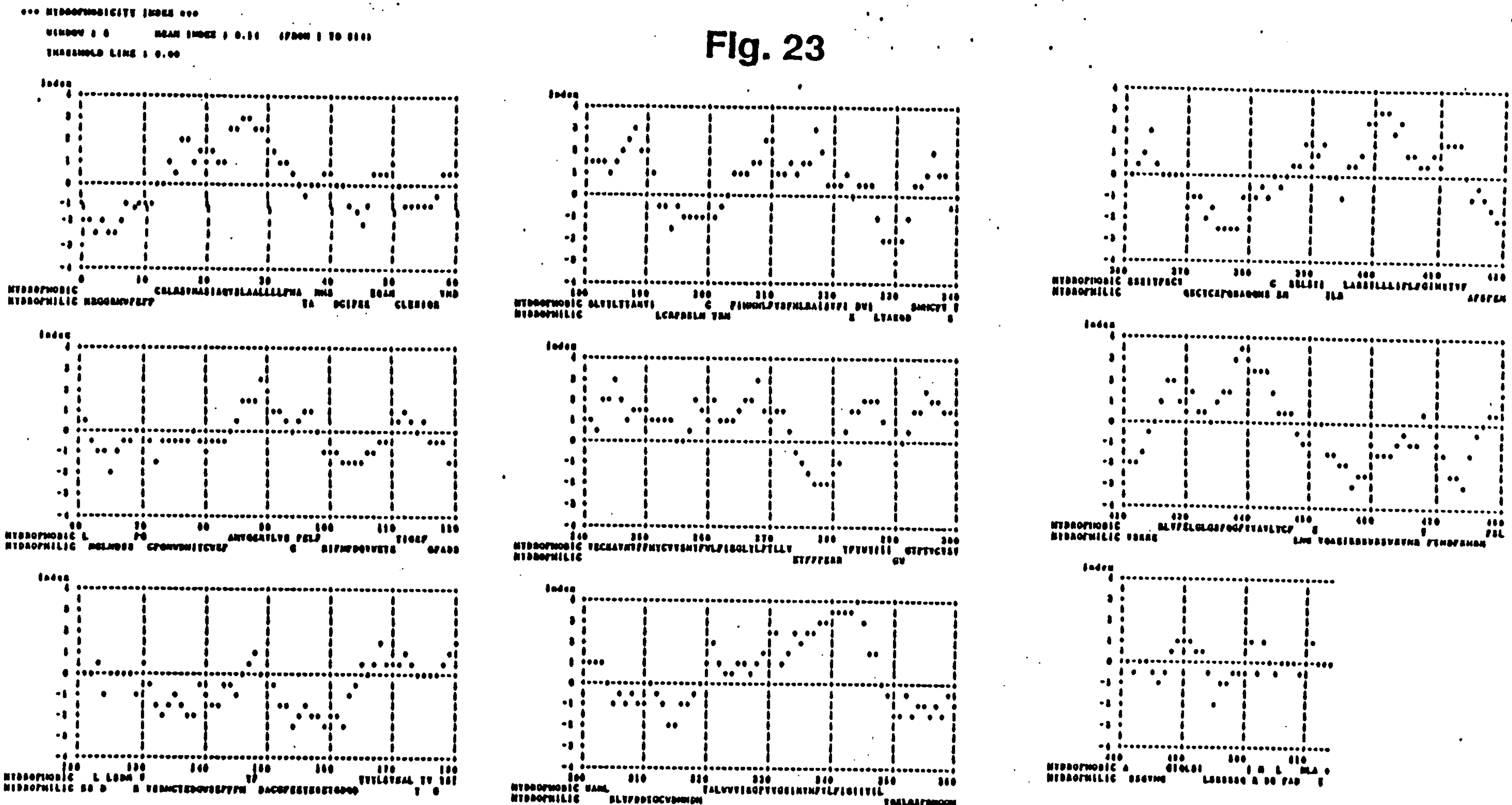

Fig. 23

Fig. 24

DNASIS ***** HYDROPHOBICITY ANALYSIS LIST ***** DATE [illegible]

*** INPUT INFORMATION ***

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HYDROPHOBICITY INDEX TABLE FILE : [illegible]

*** HYDROPHOBICITY INDEX ***

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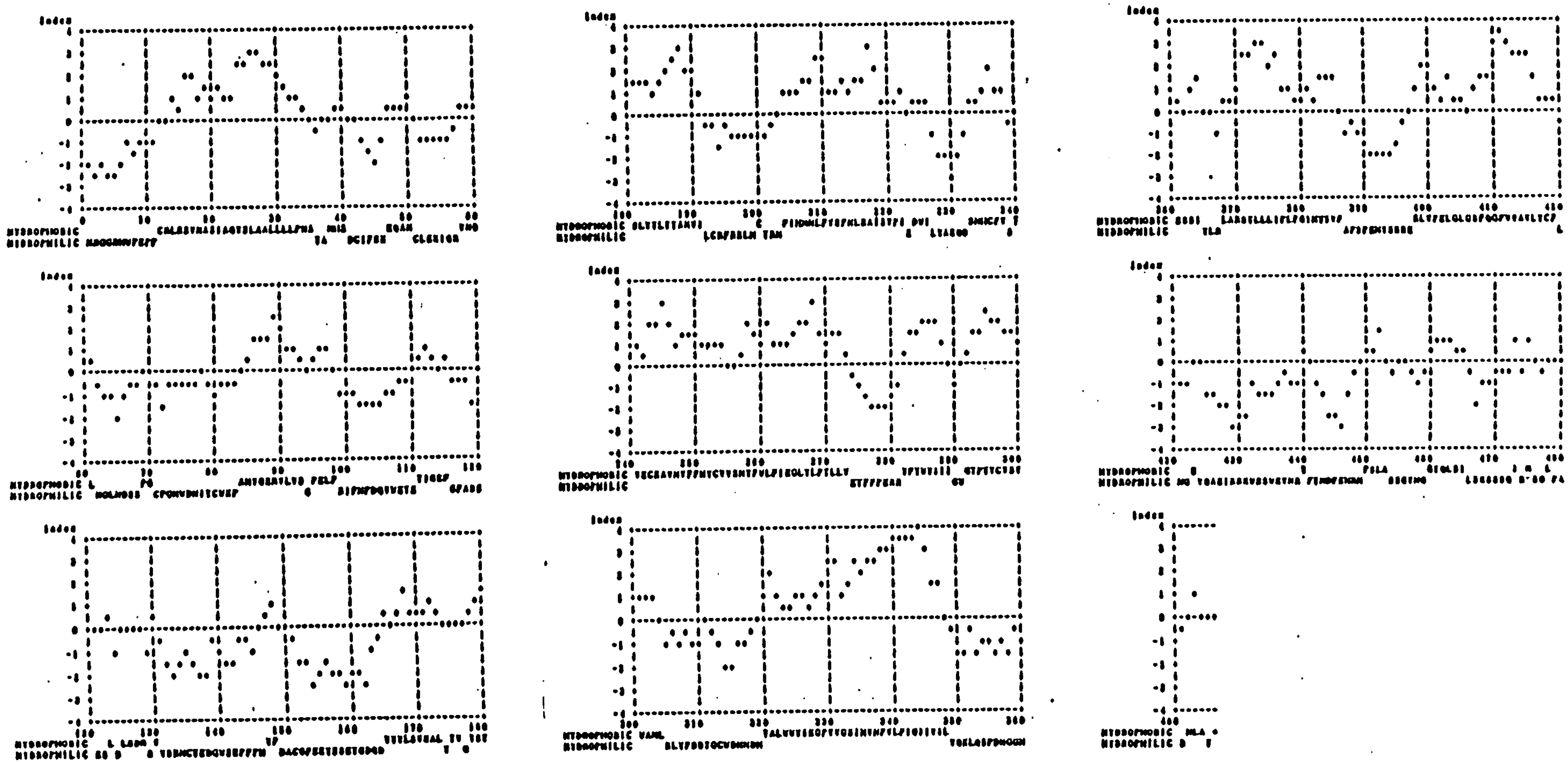


Fig. 25

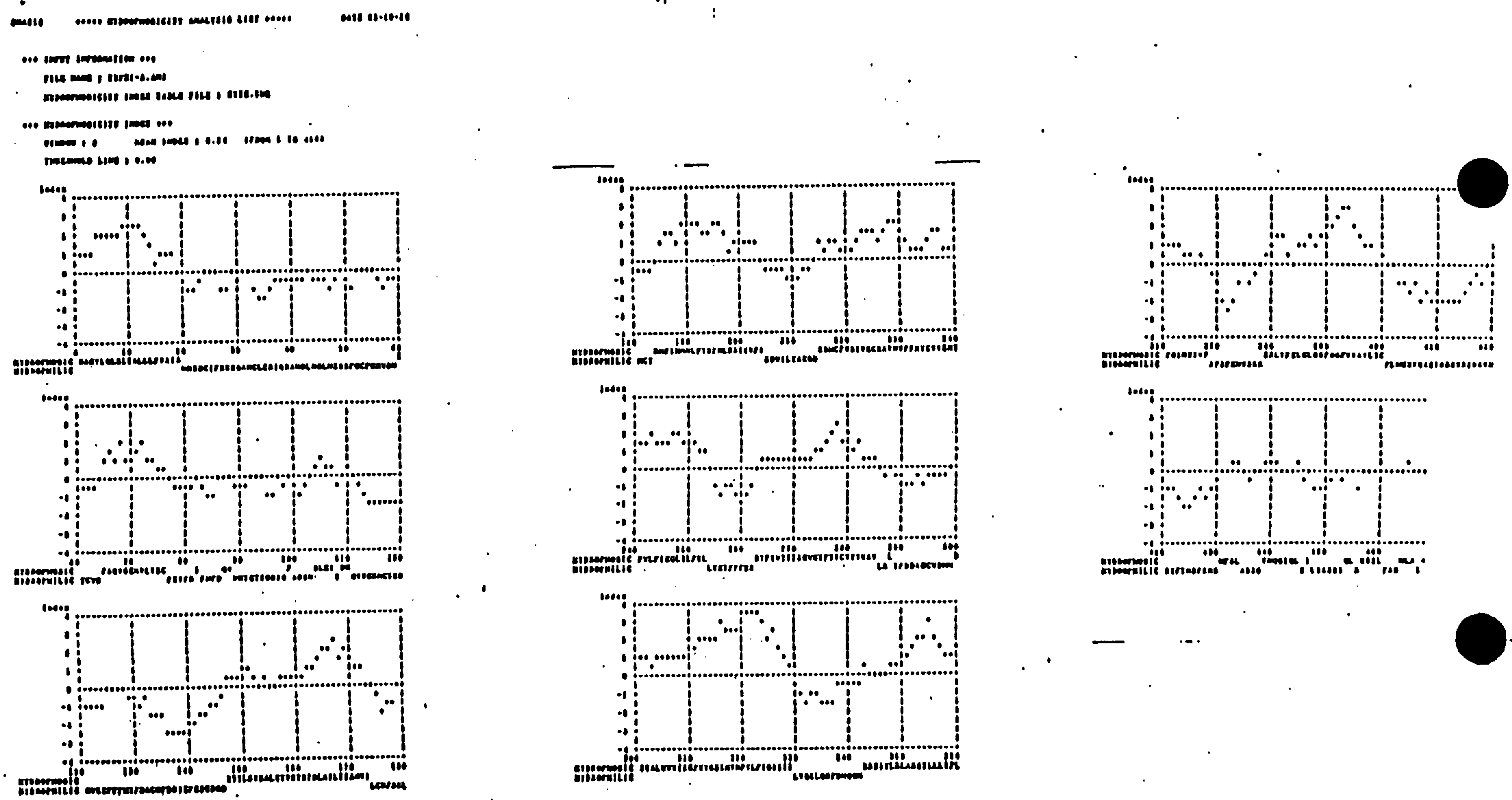


Fig. 26

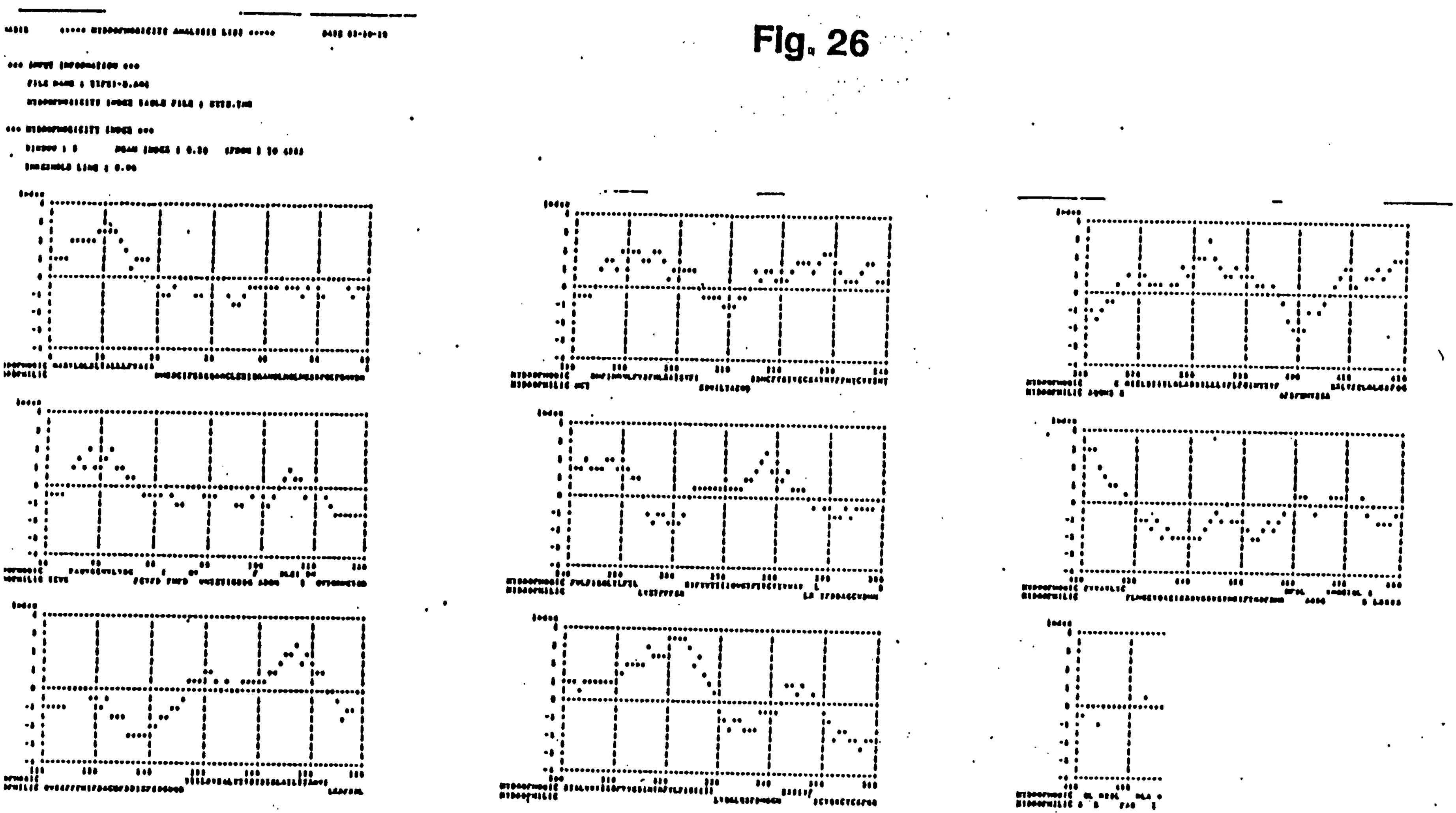


Fig. 27

***** HYDROPHOBICITY ANALYSIS LIST *****

*** INPUT INFORMATION ***

FILE NAME :

HYDROPHOBICITY INDEX TABLE FILE :

*** HYDROPHOBICITY INDEX ***

WINDOW : 5 MEAN INDEX : 0.10 (FROM 1 TO 555)

THRESHOLD LINE : 0.00

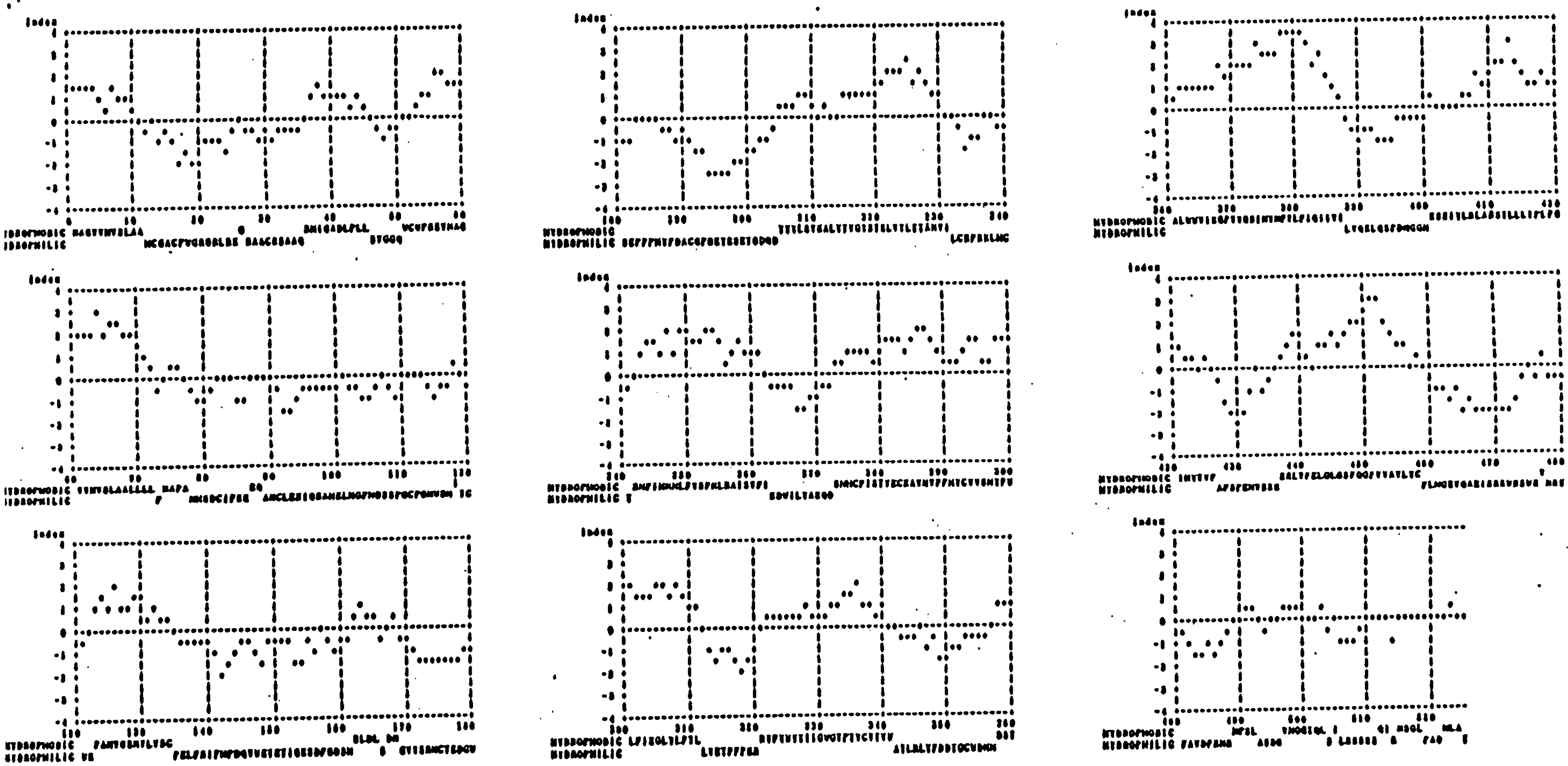


Fig. 28

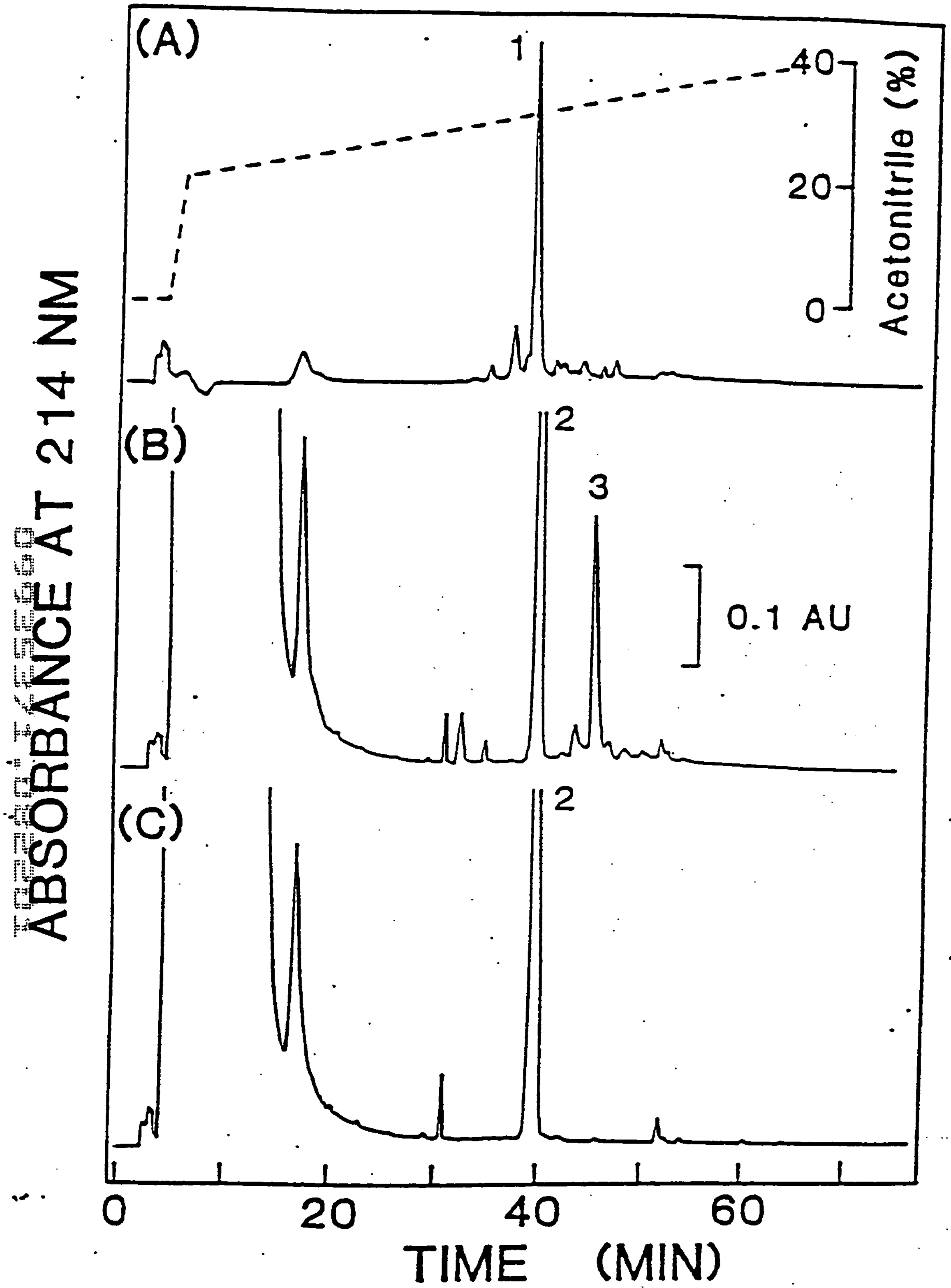
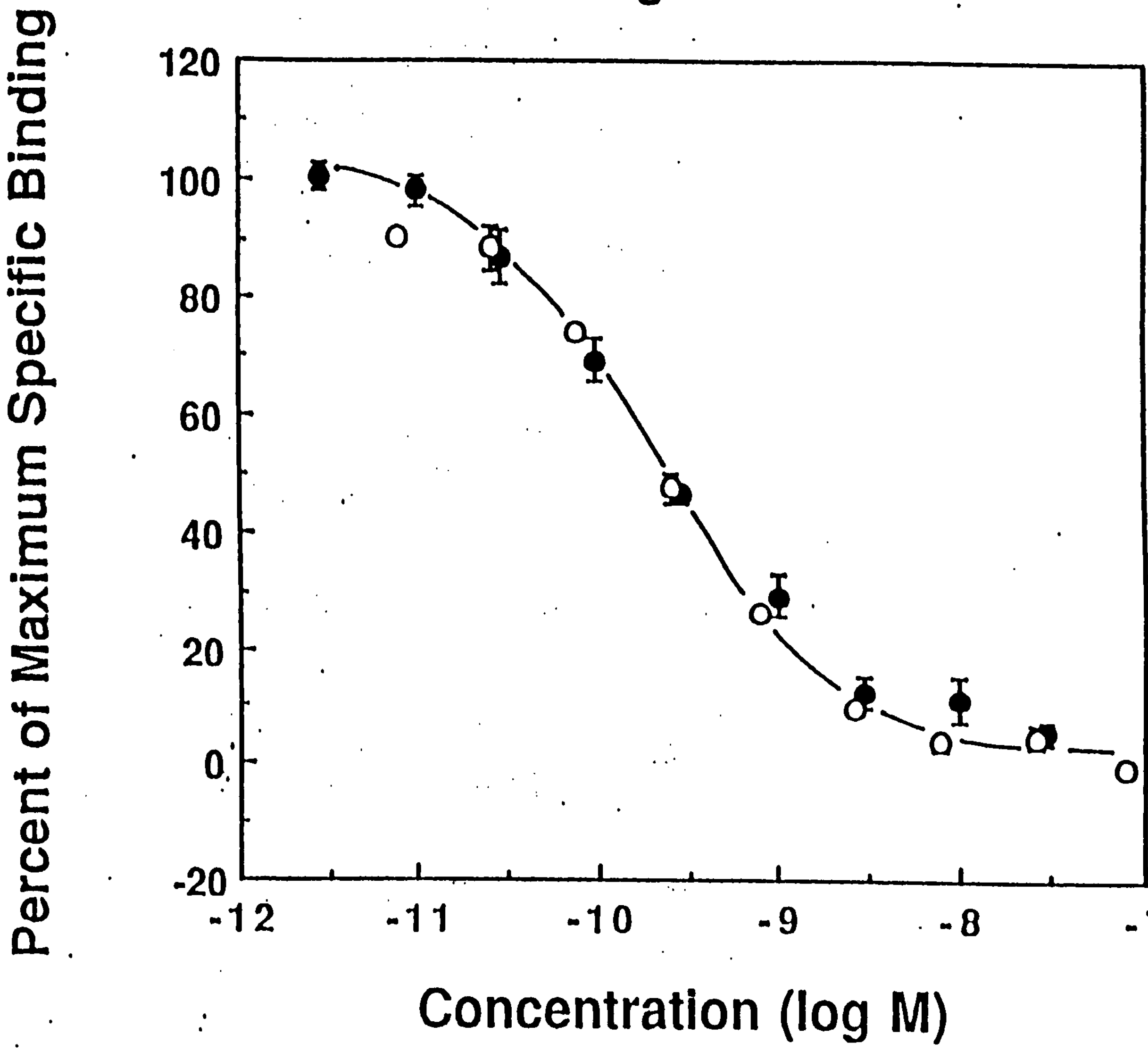

(A)
1
40
20
0
Acetonitrile (%)
(B)
2
3
0.1 AU
(C)
2
ABSORBANCE AT 214 NM
0
20
40
60
TIME (MIN)

Fig. 29



Percent of Maximum Specific Binding
120
100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
Concentration (log M)

Fig. 30

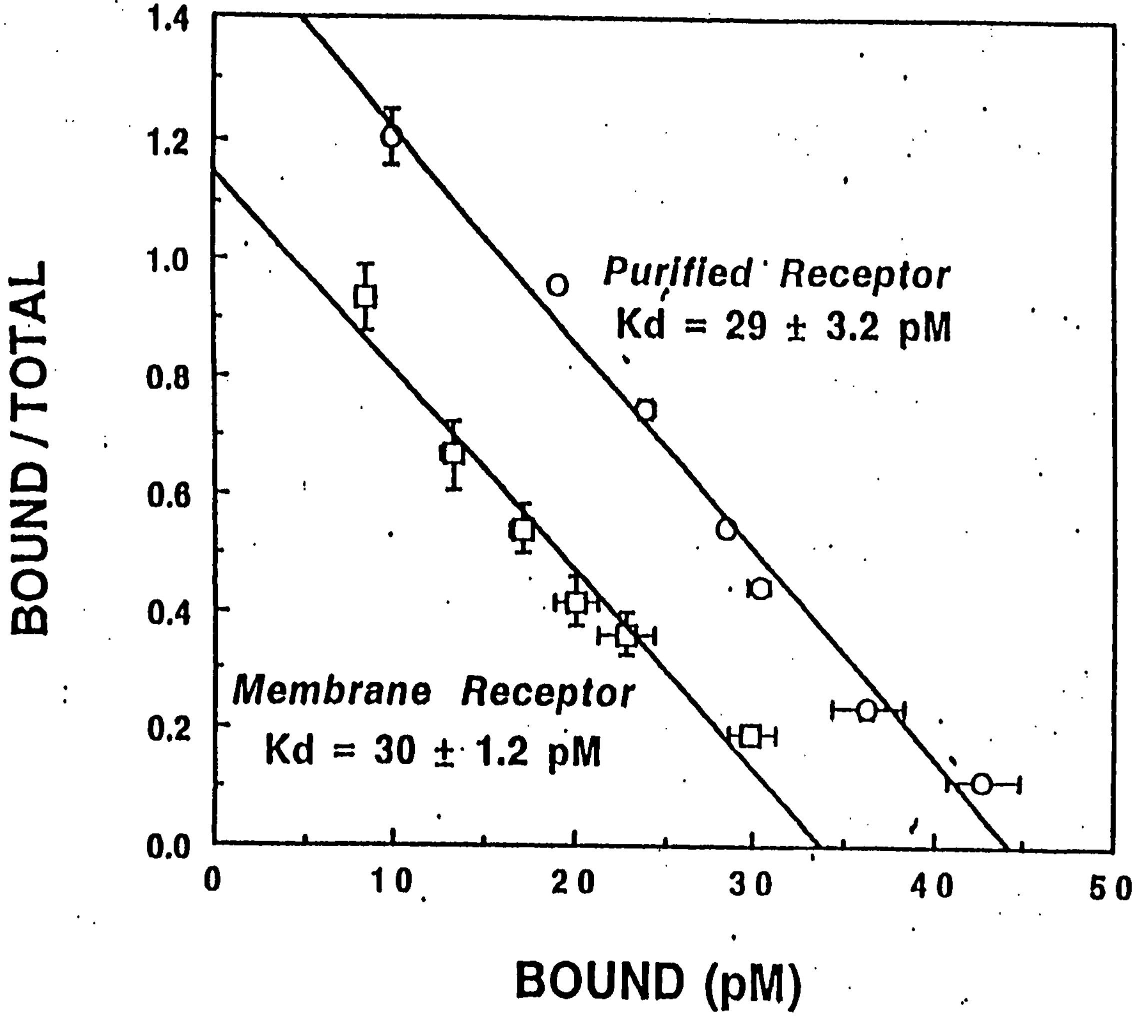

Purified Receptor
Kd = 29 ± 3.2 pM
Membrane Receptor
Kd = 30 ± 1.2 pM
BOUND / TOTAL
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
BOUND (pM)

Fig. 31

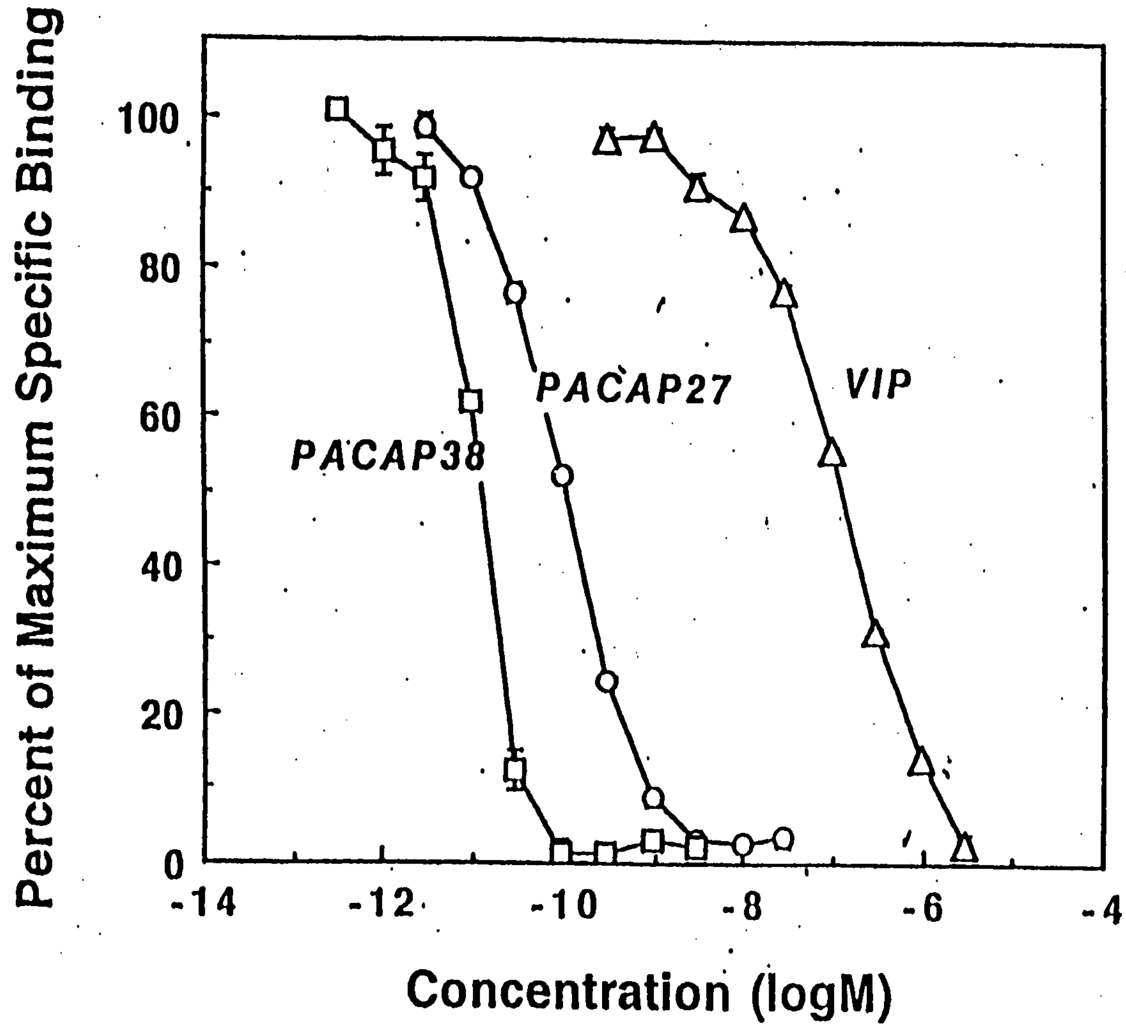

Percent of Maximum Specific Binding
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
Concentration (logM)
PACAP38
PACAP27
VIP

Fig. 32

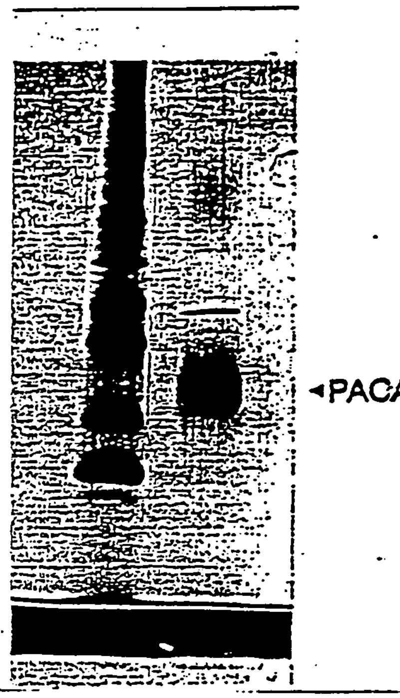
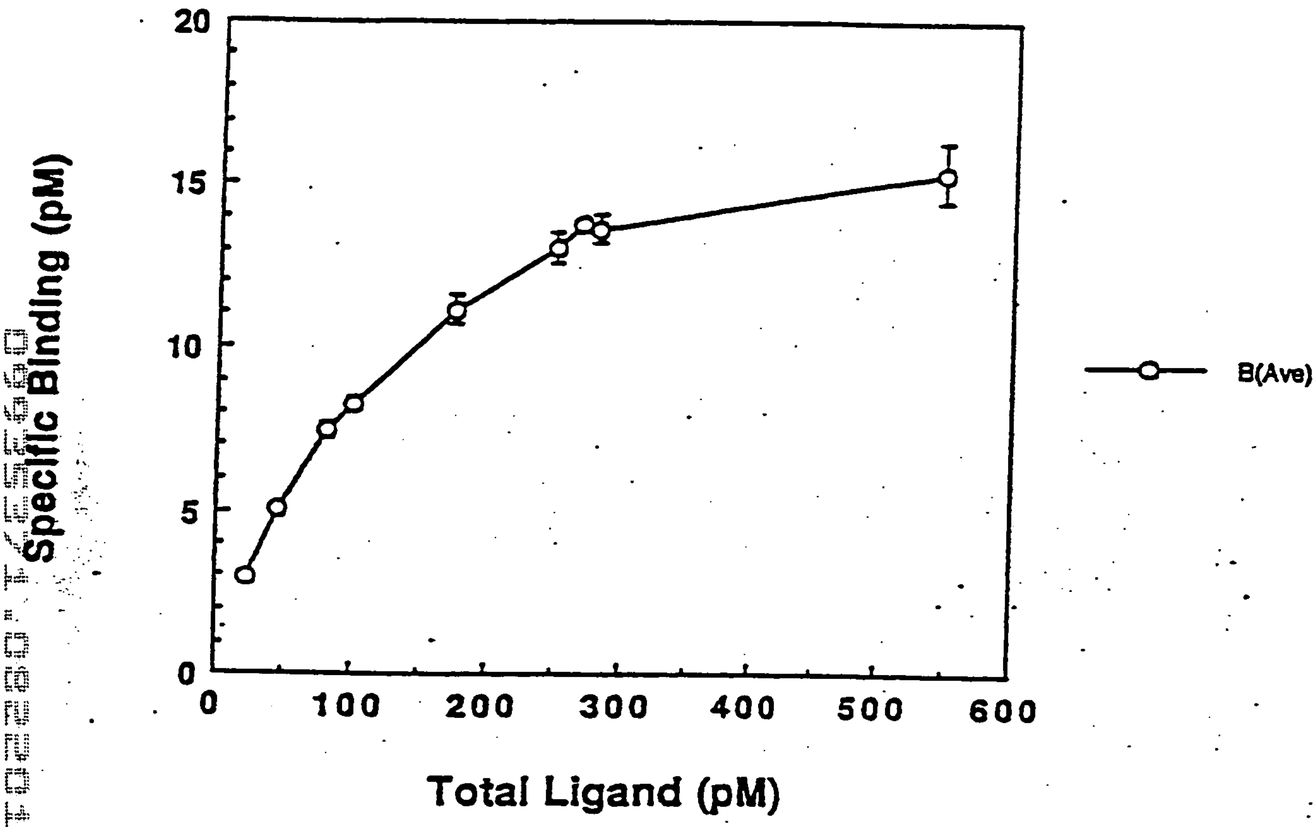


Fig. 33



Specific Binding (pM)
20
15
10
5
0
0
100
200
300
400
500
600
Total Ligand (pM)
B(Ave)

Fig. 34

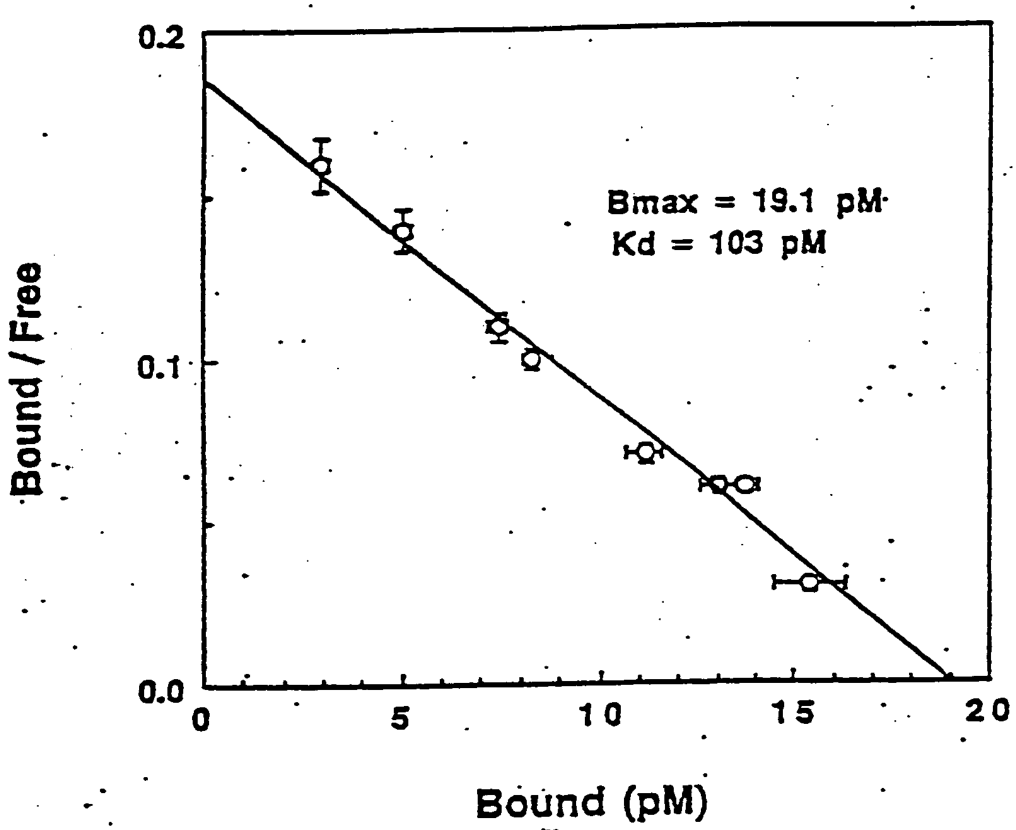
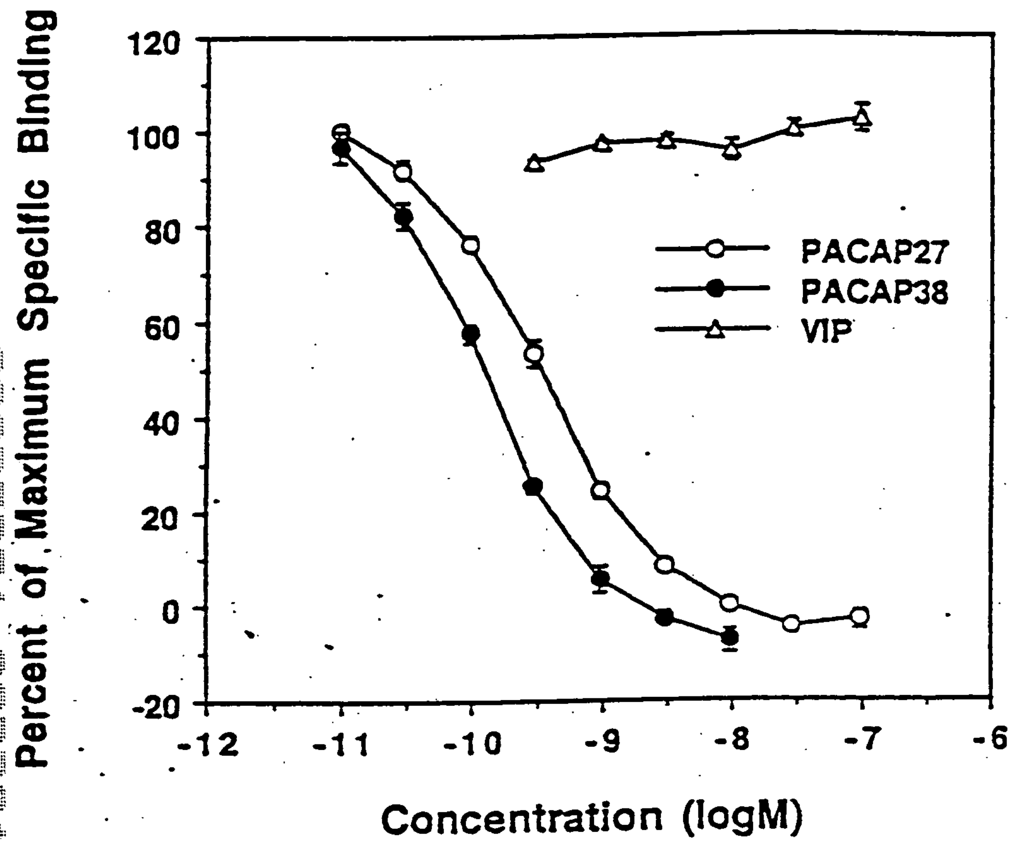
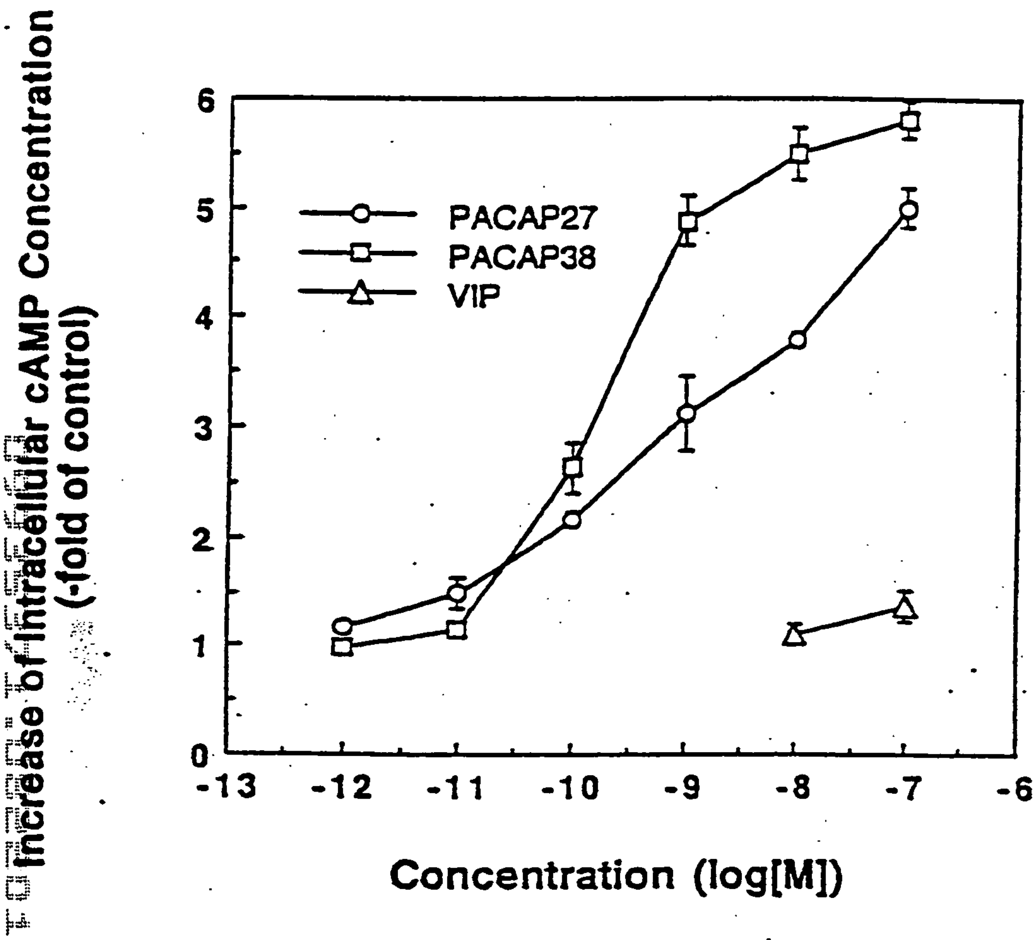


Fig. 35



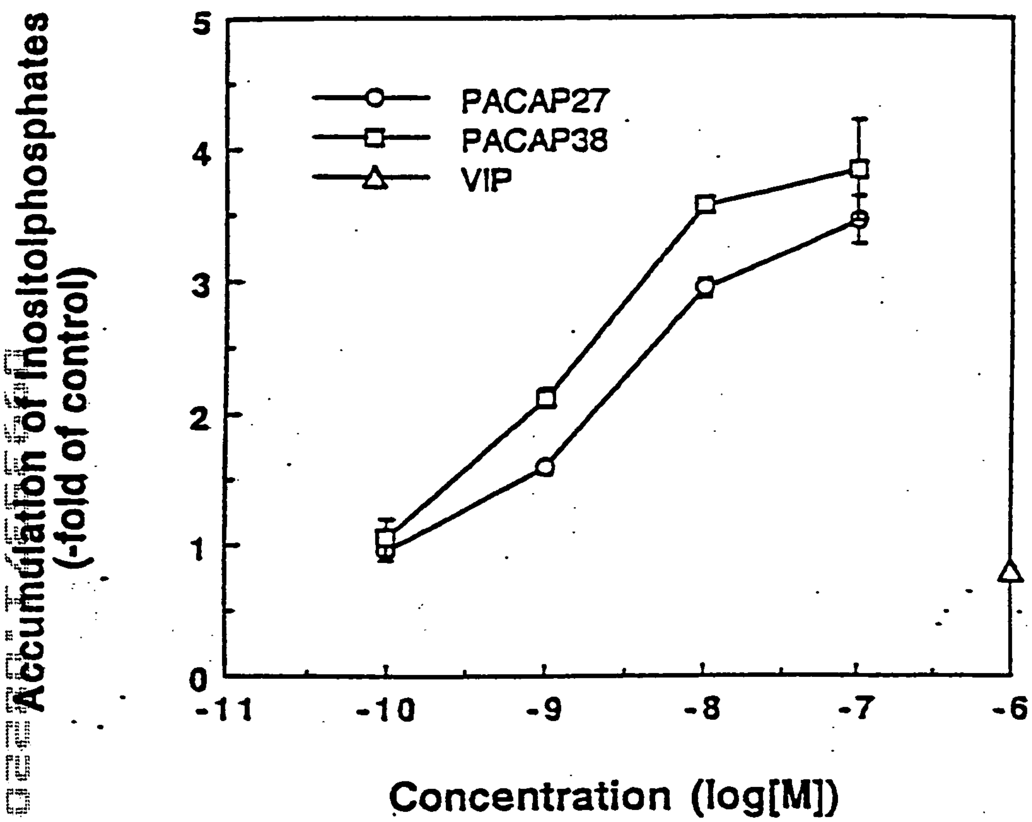
120
100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
-6
Percent of Maximum Specific Binding
Concentration (logM)
PACAP27
PACAP38
VIP

Fig. 36



Increase of Intracellular cAMP Concentration
(-fold of control)
PACAP27
PACAP38
VIP
6
5
4
3
2
1
0
-13
-12
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 37



Accumulation of inositolphosphates (-fold of control)
5
4
3
2
1
0
PACAP27
PACAP38
VIP
-11
-10
-9
-8
-7
-6
Concentration (log[M])

Fig. 38

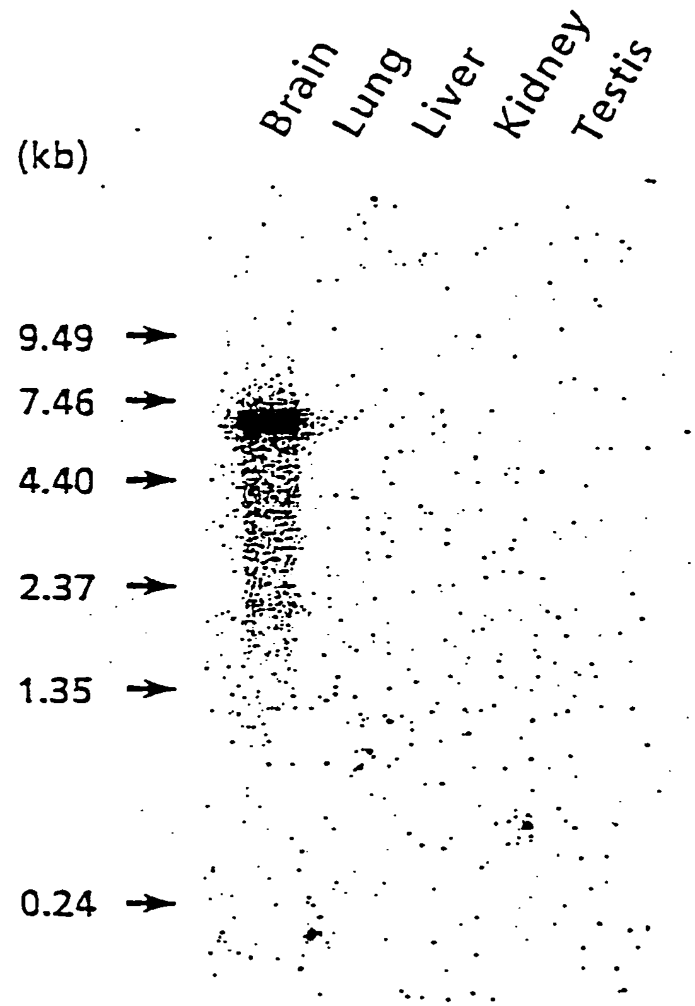
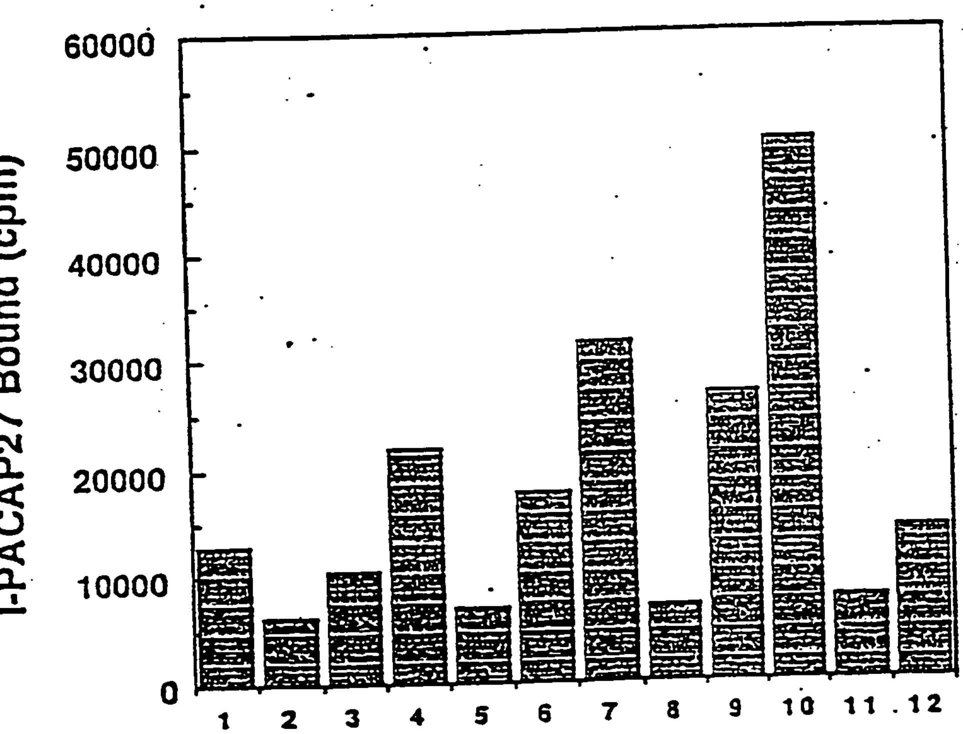


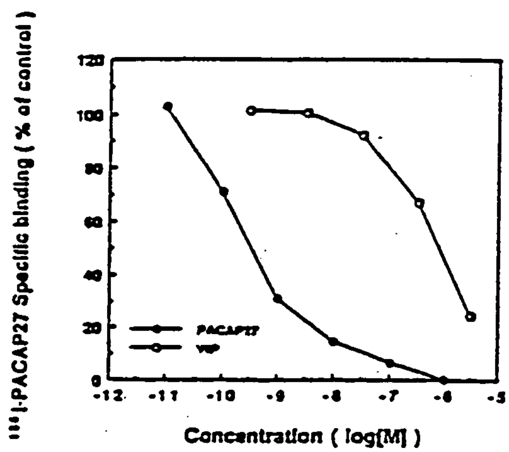
Fig. 39



I-PACAP27 Bound (cpm)
60000
50000
40000
30000
20000
10000
0
1
2
3
4
5
6
7
8
9
10
11
12

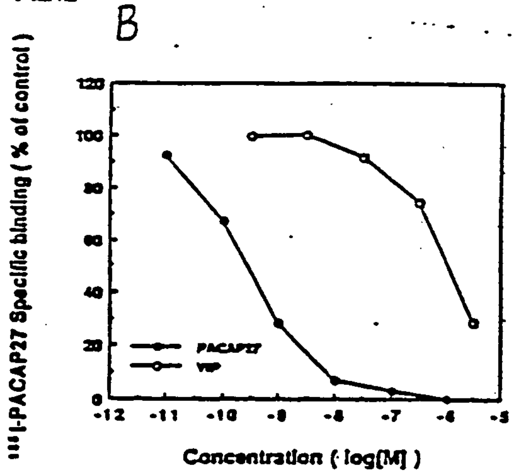
Fig. 40

A



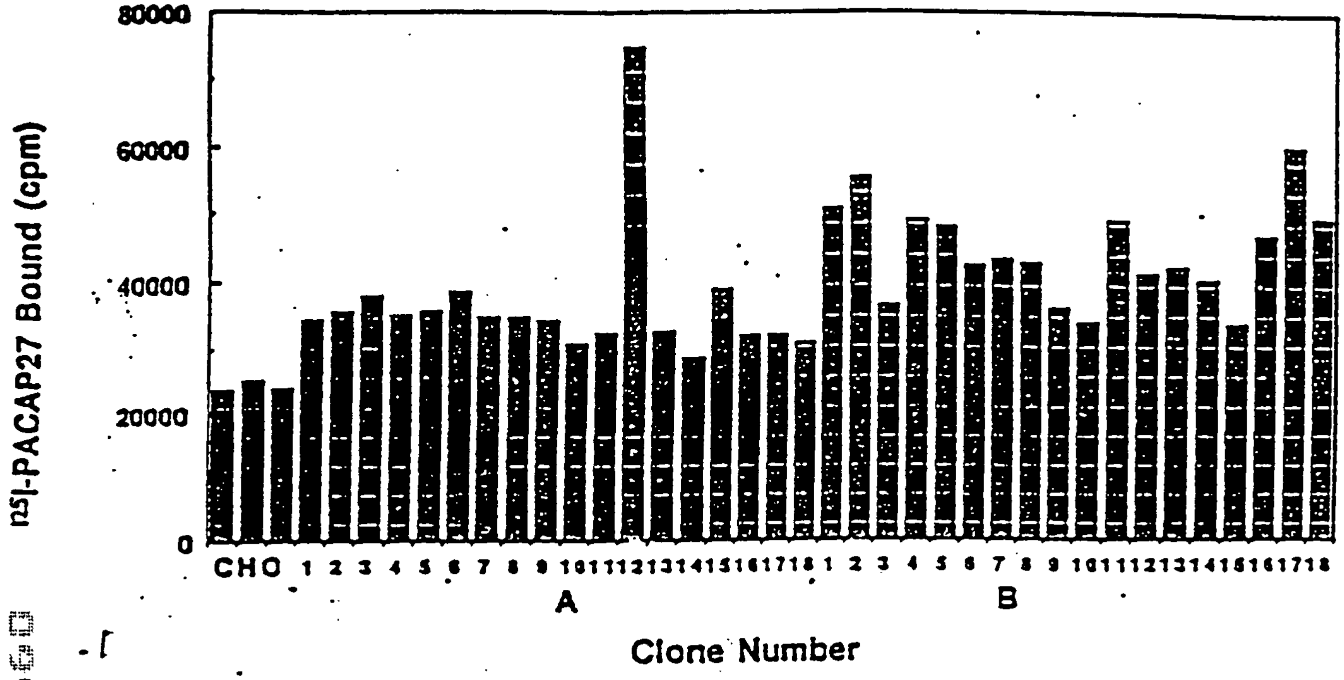
125I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])

B



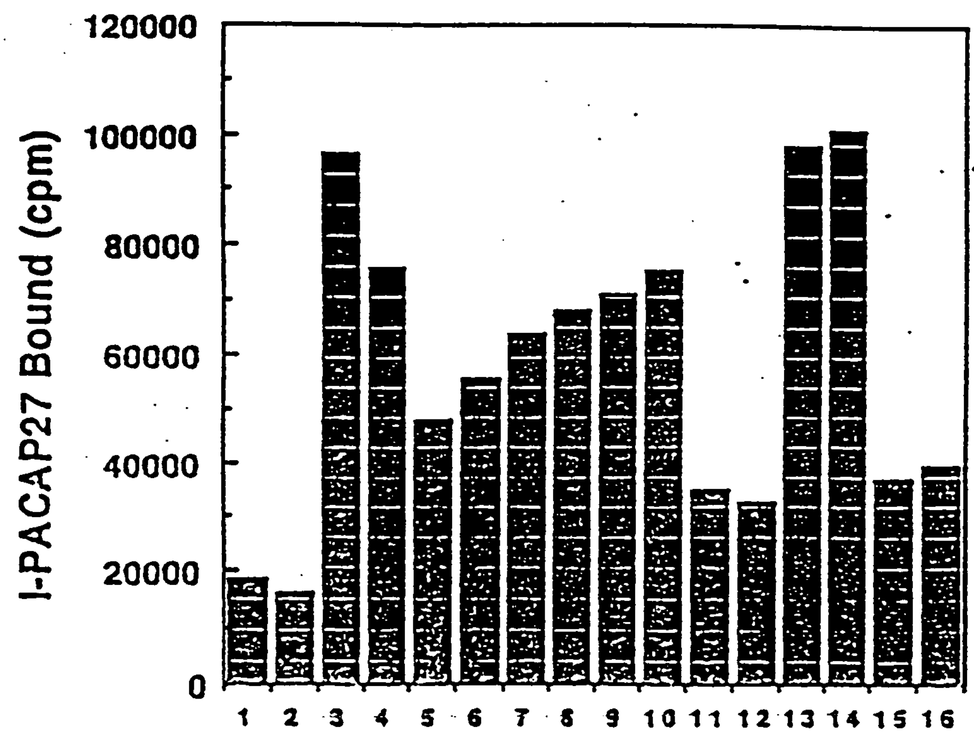
125I-PACAP27 Specific binding (% of control)
120
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
-5
PACAP27
VIP
Concentration (log[M])

Fig. 41



125I-PACAP27 Bound (cpm)
80000
60000
40000
20000
0
CHO 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
A
B
Clone Number

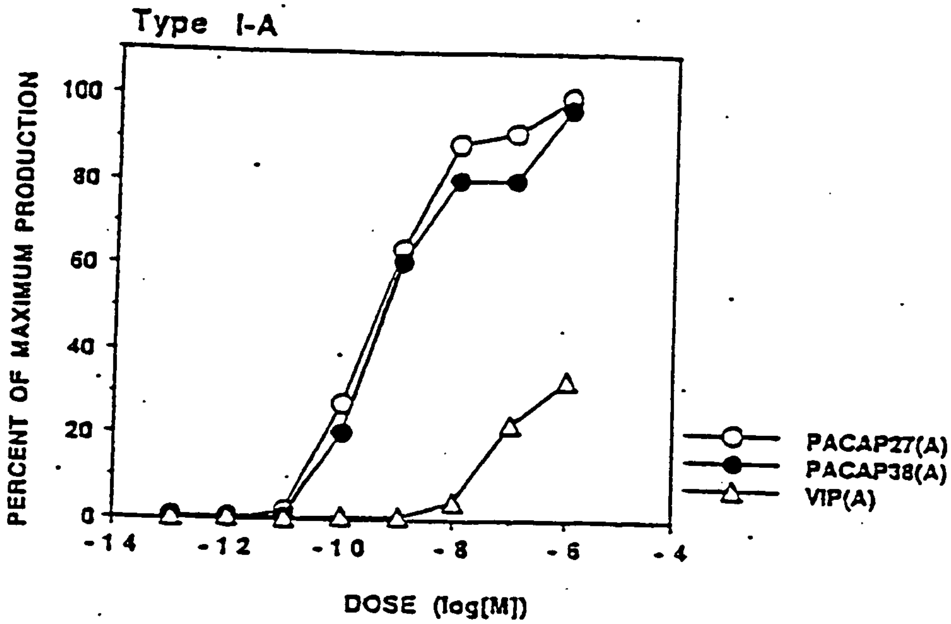
Fig. 42



I-PACAP27 Bound (cpm)
120000
100000
80000
60000
40000
20000
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

No. ....

Fig. 43


Type I-A
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(A)
PACAP38(A)
VIP(A)

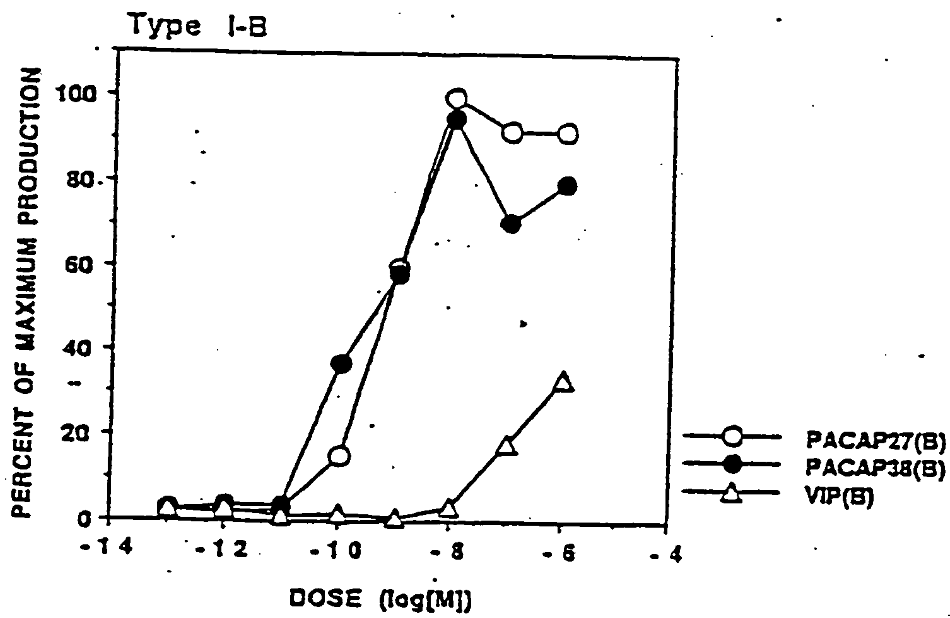

Type I-B
PERCENT OF MAXIMUM PRODUCTION
100
80
60
40
20
0
-14
-12
-10
-8
-6
-4
DOSE (log[M])
PACAP27(B)
PACAP38(B)
VIP(B)

Fig. 44

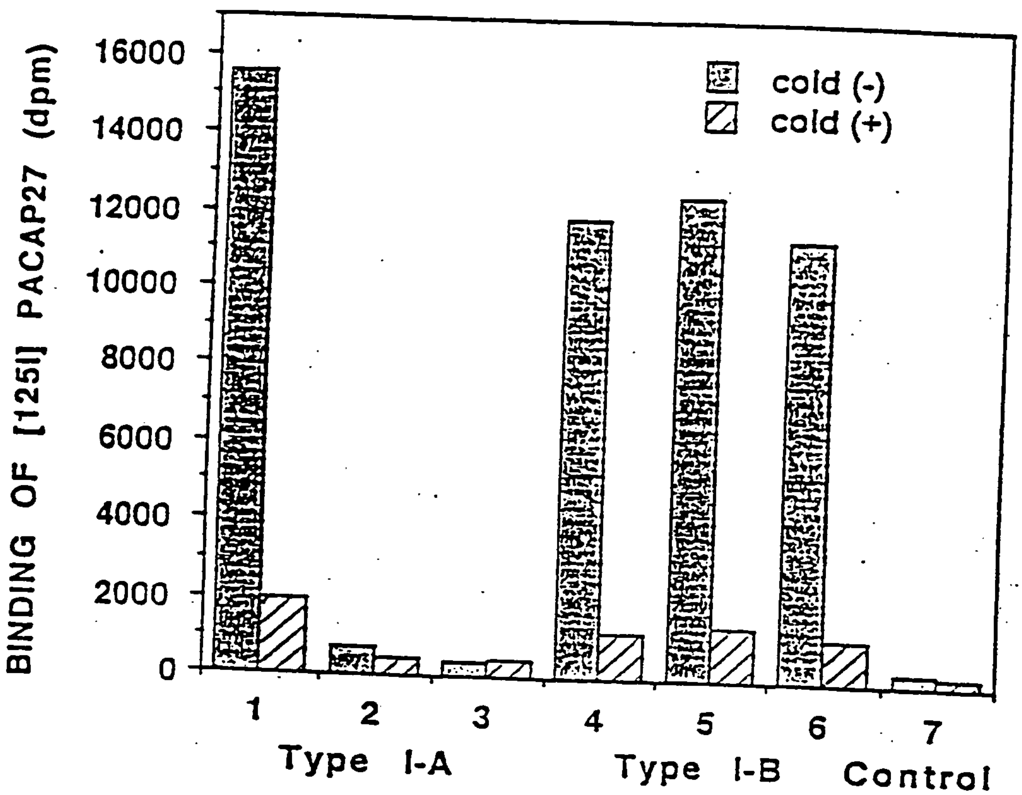
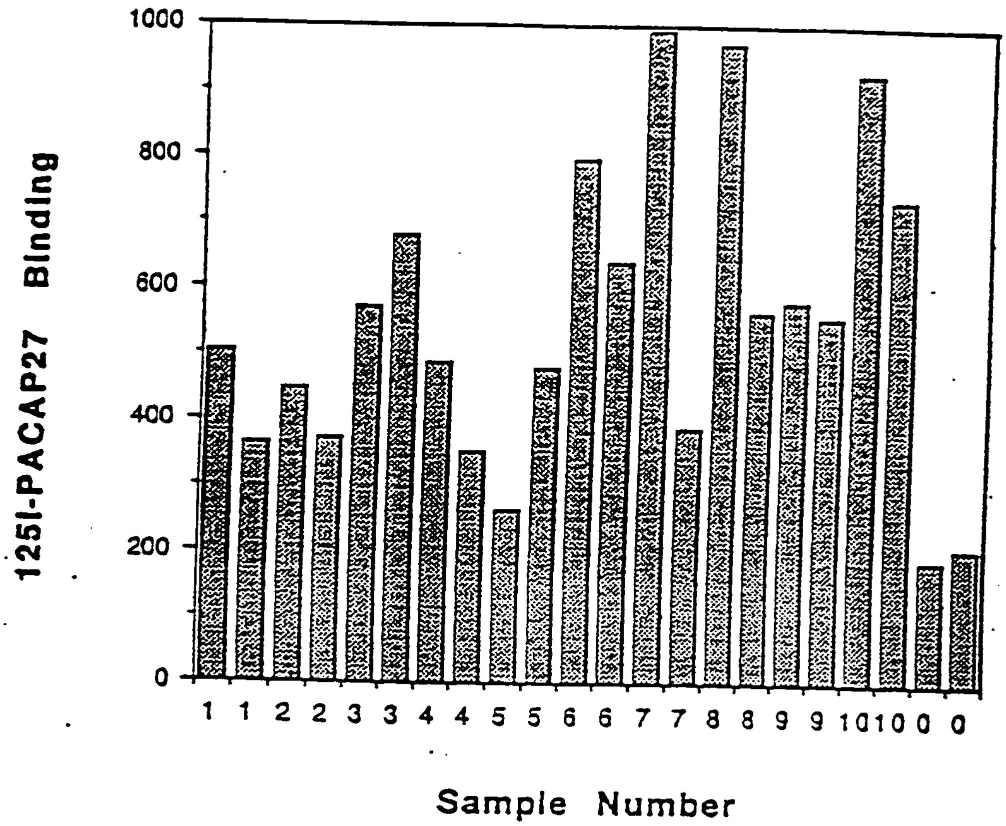

BINDING OF [125I] PACAP27 (dpm)
16000
14000
12000
10000
8000
6000
4000
2000
0
cold (-)
cold (+)
1
2
3
4
5
6
7
Type I-A
Type I-B
Control

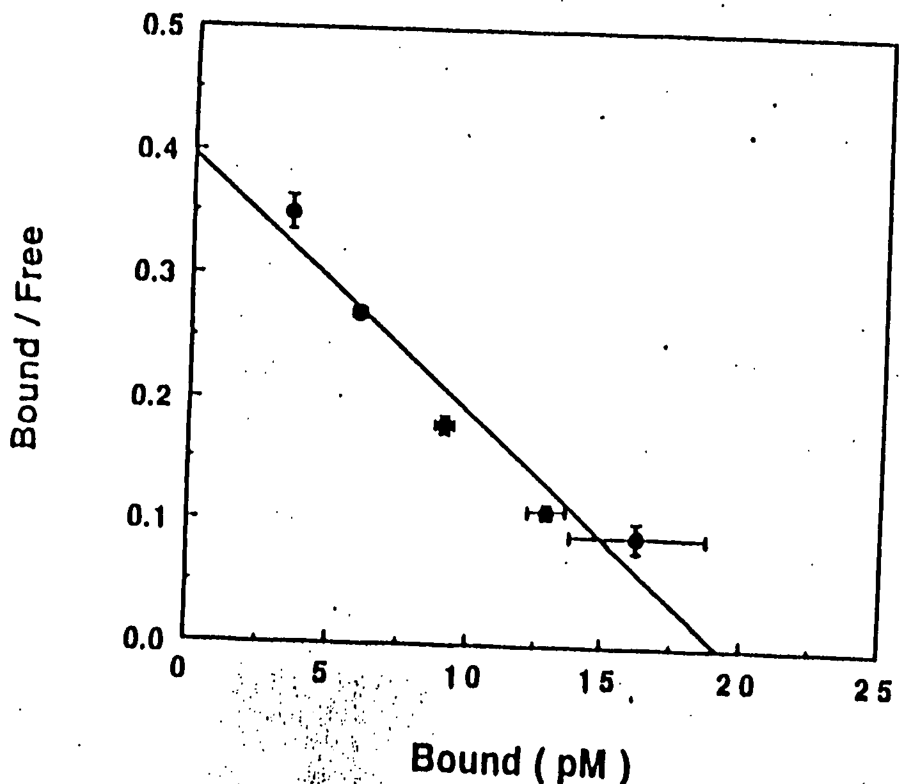
Fig. 45



125I-PACAP27 Binding
1000
800
600
400
200
0
1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 0 0
Sample Number

A

Fig. 46



B

Fig. 47

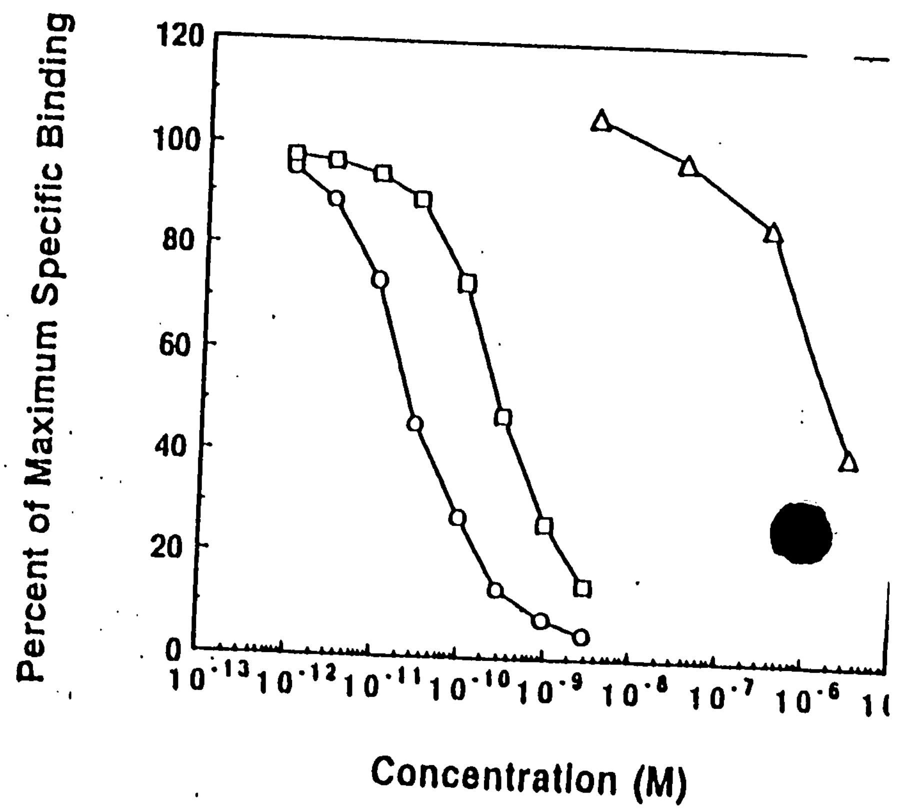
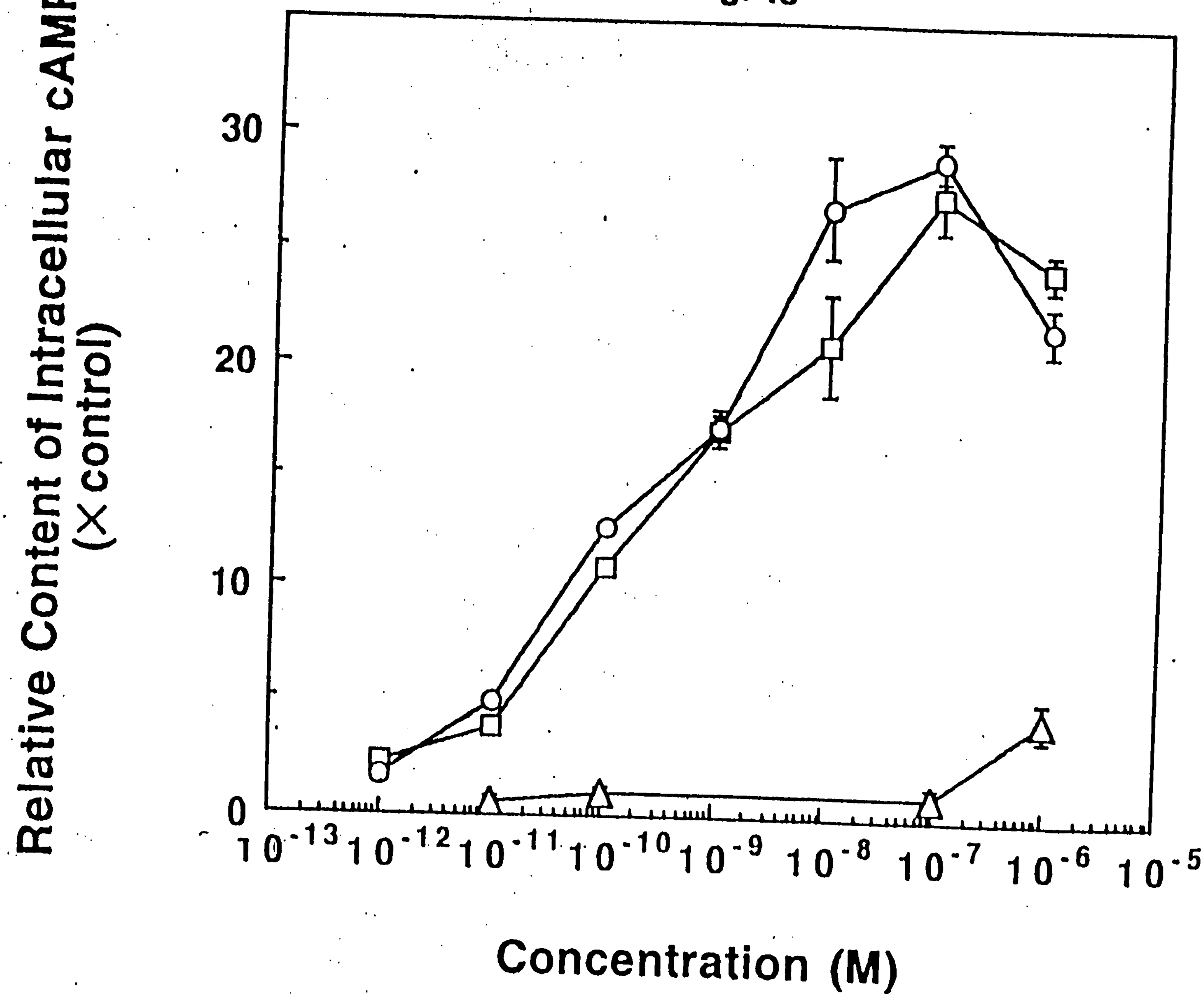


Fig. 48



Relative Content of Intracellular cAMP
(×control)
30
20
10
0
10^{-13}
10^{-12}
10^{-11}
10^{-10}
10^{-9}
10^{-8}
10^{-7}
10^{-6}
10^{-5}
Concentration (M)

Fig. 49

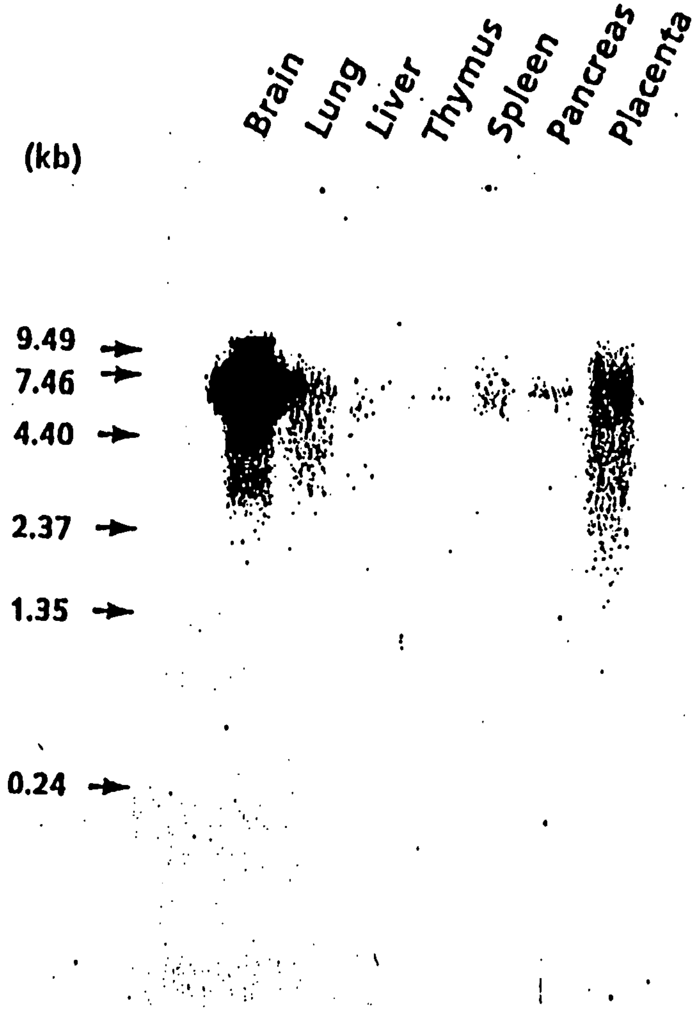

(kb)
9.49
7.46
4.40
2.37
1.35
0.24
Brain
Lung
Liver
Thymus
Spleen
Pancreas
Placenta

Fig. 50

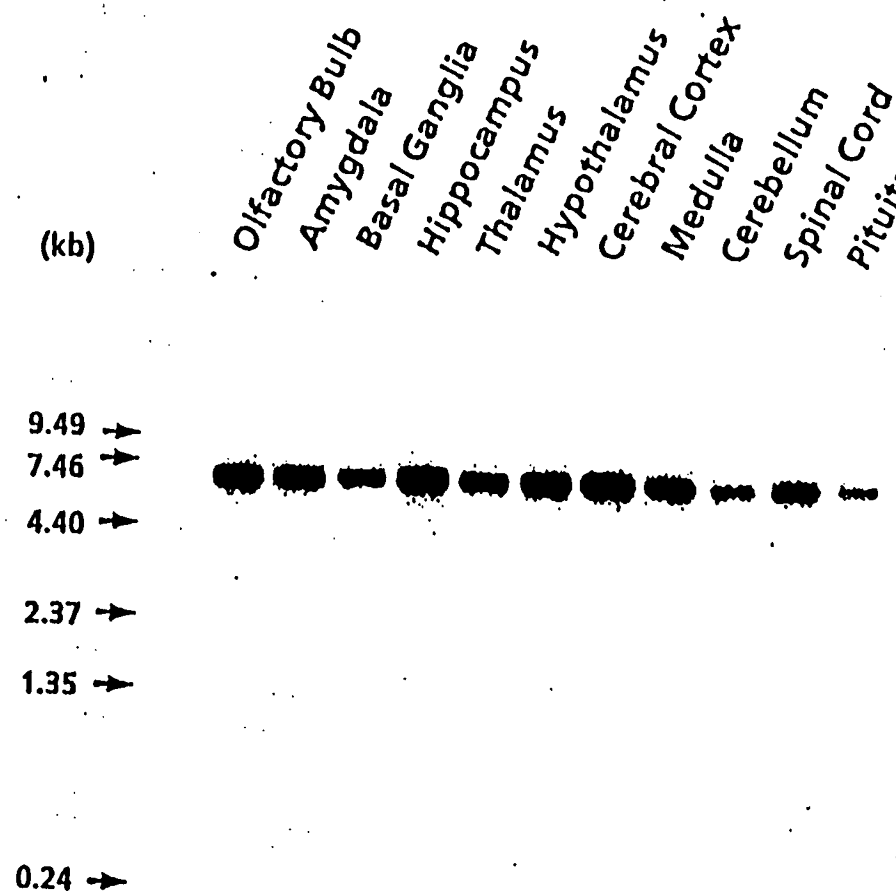
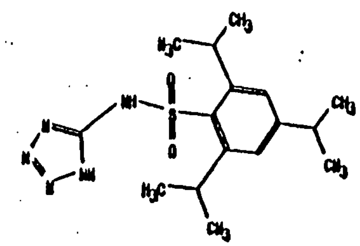
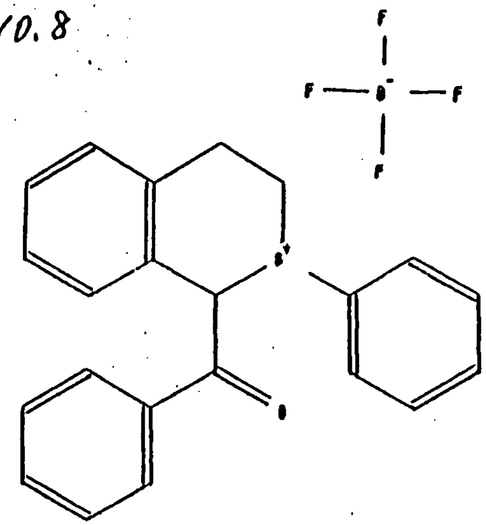

(kb)
9.49
7.46
4.40
2.37
1.35
0.24
Olfactory Bulb
Amygdala
Basal Ganglia
Hippocampus
Thalamus
Hypothalamus
Cerebral Cortex
Medulla
Cerebellum
Spinal Cord
Pituitary

Fig. 51-2

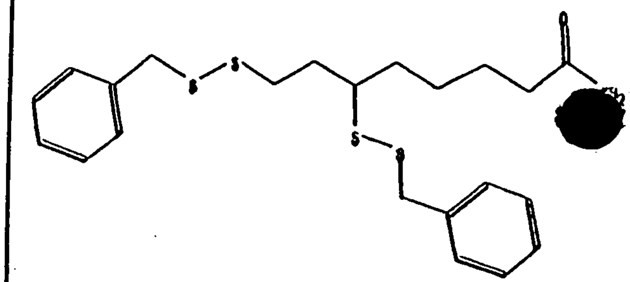
NO.7



NO.8



NO.9



NO.10

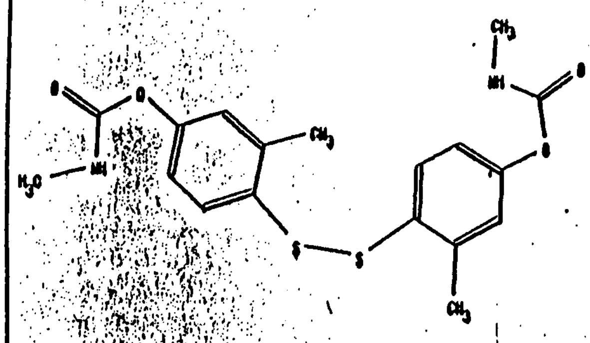
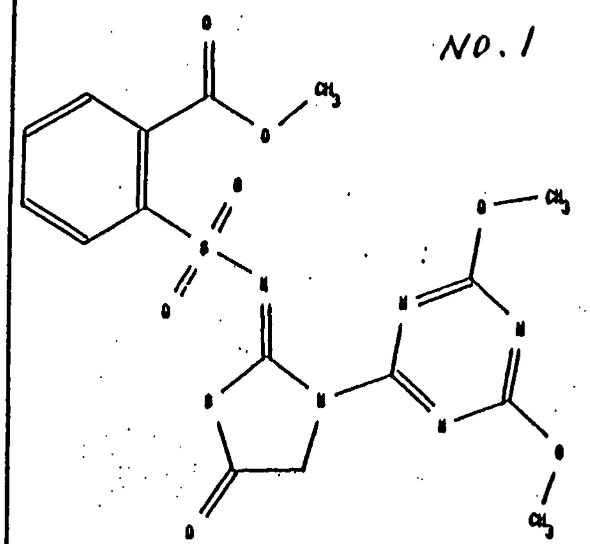
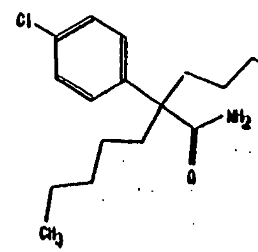


Fig. 51-1

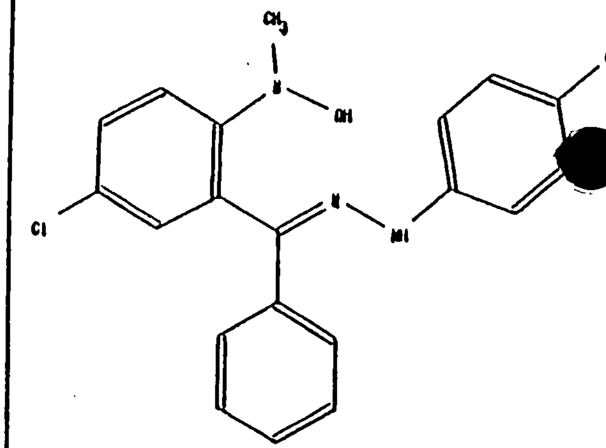
NO. 1



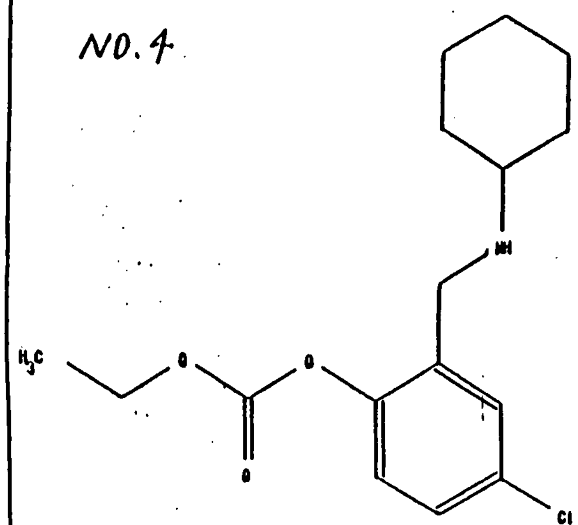
NO. 2



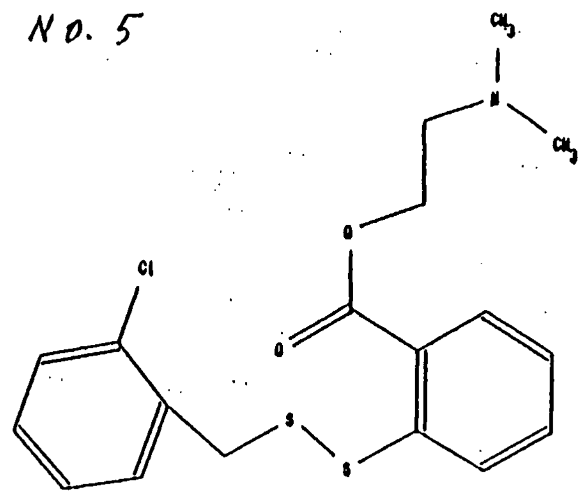
NO. 3



NO. 4



NO. 5



NO. 6

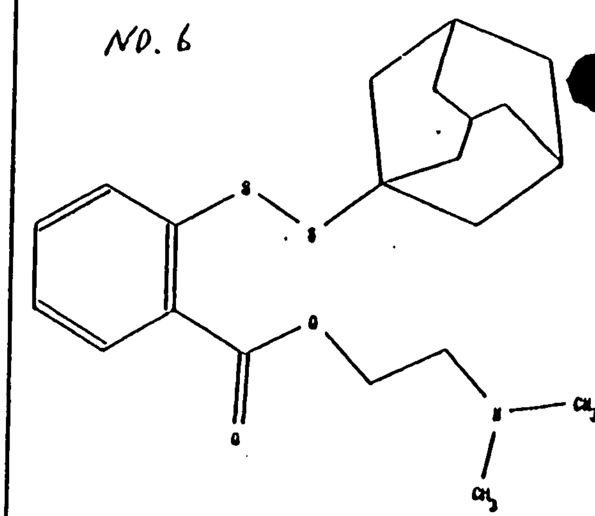
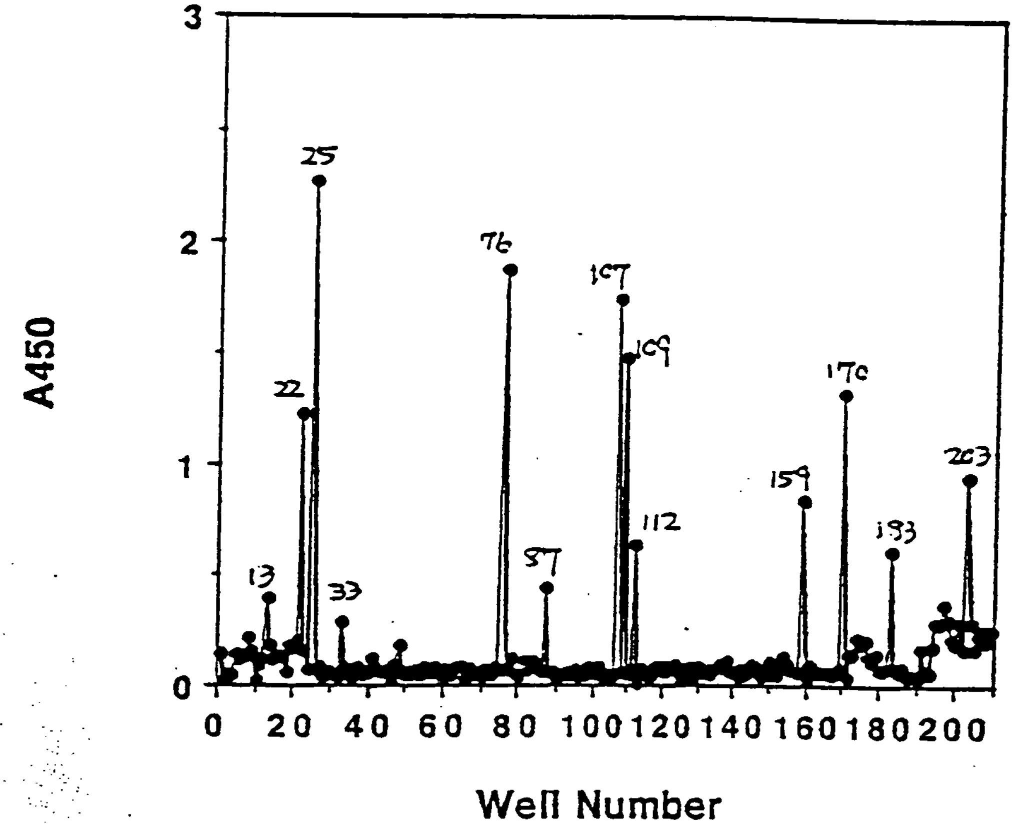


Fig. 52



3
2
1
0
A450
25
76
107
109
22
170
203
159
112
193
87
13
33
0
20
40
60
80
100
120
140
160
180
200
Well Number

Fig. 53

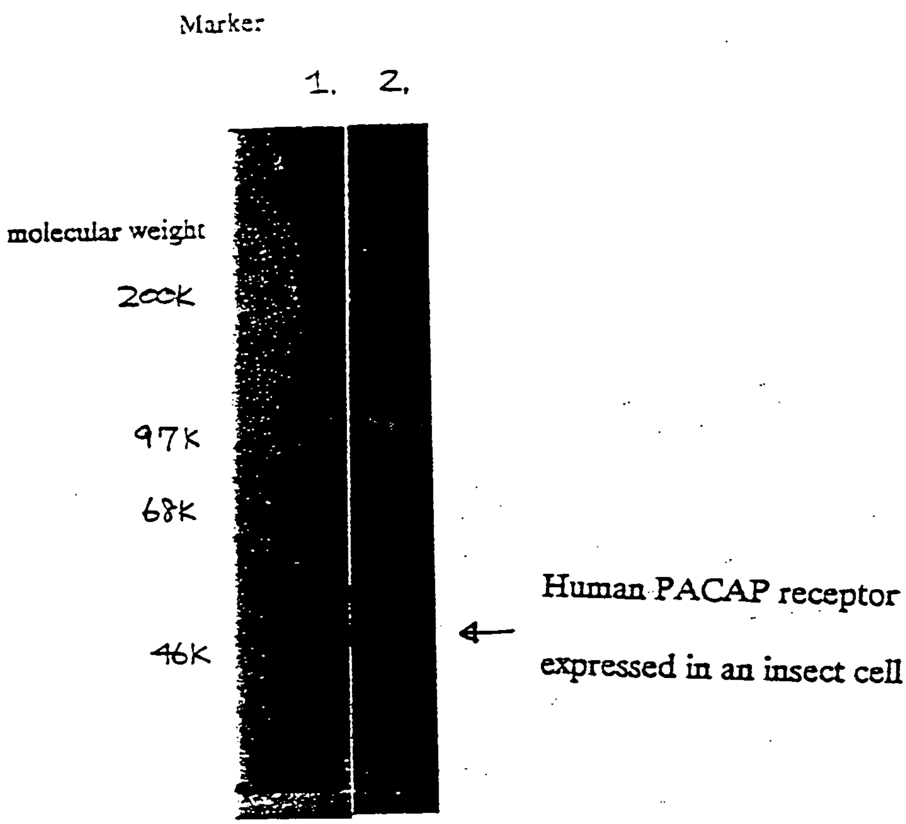
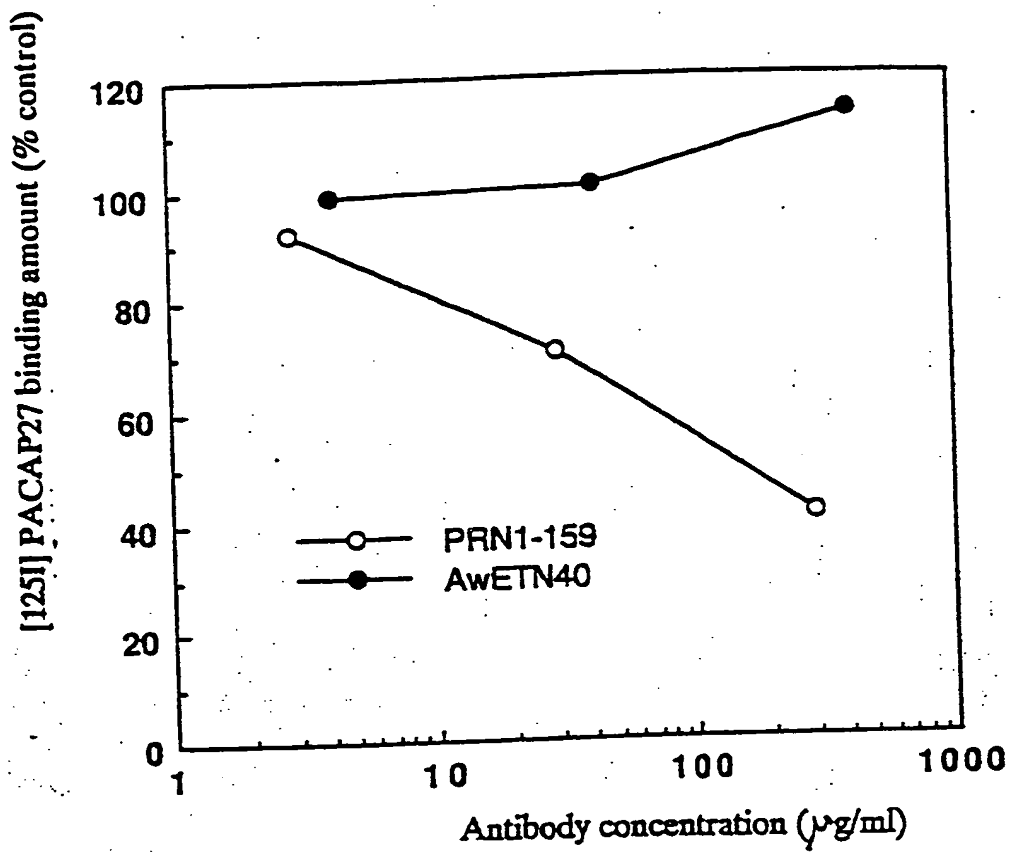

Marker
1.
2.
molecular weight
200K
97K
68K
46K
Human PACAP receptor
expressed in an insect cell

Fig. 54


[125I] PACAP27 binding amount (% control)
120
100
80
60
40
20
0
1
10
100
1000
Antibody concentration (μg/ml)
PRN1-159
AwETN40